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OM nucleic - nucleic search, using sw model

Run on: August 23, 2003, 05:28:22 ; Search time 1928 Seconds
(without alignments)
6378.664 Million cell updates/sec

Title: US-09-854-562-1

Perfect score: 506
Sequence: 1 aaagagacatgctgctgttc.....aaaaaaaaaaaaaaaaaaaaa 506

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hc: *
9: gb_est1: *
10: gb_est2: *
11: gb_hc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: em_gss_hum: *
18: em_gss_inv: *
19: em_gss_pln: *
20: em_gss_vit: *
21: em_gss_fun: *
22: em_gss_mam: *
23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_rtd: *
26: em_gss_phg: *
27: em_gss_vr1: *
28: gb_gss1: *
29: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	494.4	97.7	633	14	CB164987 KS0600583
2	486	96.0	530	12	BM062133 KS01038H0
3	459	90.7	527	12	BM064680 KS01070A0
4	443.2	87.6	648	14	CB185066 KS04236T7

5	440.8	87.1	506	14	CB164889 KS050143T
6	421	83.2	496	14	CB164824 KS050003T
7	378	74.7	540	12	BM063527 KS01056D1
8	376.4	74.4	580	12	BM065064 KS01074E1
9	372.2	73.6	720	14	CB185076 KS04192T7
10	364	71.9	545	14	CA525505 KS12056G0
11	363.8	71.9	448	12	BM063616 KS01057B0
12	363.6	71.9	535	12	BM062737 KS01046F0
13	360	71.1	571	14	CA515866 KS09048E1
14	356.8	70.5	537	14	BM064540 KS01068D0
15	353.6	69.9	522	12	BM064663 KS01069H0
16	353.6	69.9	531	12	BM063609 KS01057D1
17	345.2	68.2	521	14	CA524161 KS12033G0
18	343.2	67.8	416	14	CB164909 KS050169T
19	339.6	67.1	509	12	BM061371 KS01029G1
20	321.2	63.5	474	14	CA525605 KS12058F0
21	302.8	59.8	481	12	BM064286 KS01065D0
22	291.8	57.7	466	12	BM063884 KS01060F0
23	286.2	56.6	447	14	CA524497 KS12038D0
24	284.6	56.2	474	14	CA514352 KS09023C0
25	281.6	51.7	672	12	BM064987 KS01073F0
26	254.4	50.3	332	14	CB164858 KS050090T
27	251.8	49.8	376	12	BM062401 KS01042C0
28	249.4	49.3	574	12	BM067544 KS08007B0
29	234	46.2	589	14	CA516706 KS09062G0
30	231.6	45.8	536	12	BM063253 KS01053C0
31	221	43.7	380	14	CA514462 KS09025A0
32	218.4	43.2	573	14	CA523446 KS12022C1
33	217.6	43.0	356	9	AA842822 CFF3 Fui
34	215	42.5	500	12	BM061668 KS01033C1
35	205	40.5	513	12	CA516127 KS09052A0
36	205	40.5	513	14	BM063138 KS01052A0
37	204.6	40.4	521	12	BM064471 KS01067E0
38	201	39.7	231	9	AF082706 AF082706
39	199.6	39.4	358	9	AA840730 CFF11 Fui
40	197.4	39.0	337	14	CA514064 KS09016E1
41	196	38.7	339	12	BM060748 KS01018B0
42	195	38.5	283	9	AA840727 CFF8 Fui
43	192	37.9	643	12	BM064620 KS01069C0
44	176.4	34.9	306	14	CA517625 KS09086B0
45	168.6	33.3	504	12	BM062945 KS01049C0

ALIGNMENTS

RESULT 1
LOCUS CB164987 633 bp mRNA linear EST 30-JAN-2003
DEFINITION KS06005832 KS06 Capsicum annuum CDNA, mRNA sequence.
ACCESSION CB164987
VERSION CB164987.1 GI:28151113

KEYWORDS
SOURCE
ORGANISM

Capsicum annuum
Capsicum annuum

EST.

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Capsicum.

REFERENCE 1 (bases 1 to 633)

Lee, S.J., Lee, M.Y., Lee, P.S., Choi, S.H. and Harn, C.H.

EST fragments generated by SSH of SIRO red- SIRO green/red

Unpublished

JOURNAL

COMMENT

Contact: Chee Hark Harn

Biotechnology center

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Fax: 82 31 884 7065

Email: chharn@nongwoobio.co.kr

Seq primer: T7.

Location/Qualifiers

1..633

/organism="Capsicum annuum"

FEATURES

source

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/mo1_type="mRNA"
/cultivar="SIRO"
/db_xref="taxon:4072"
/sex="hermaphrodite"
/tissue_type="Fruit"
/dev_stage="mature red, green/red"
/clone_id="KS06"
/note="Vector: pGEM-T easy; Site1: EcoRI; SIRO red - SIRO
green/red suppression subtractive cDNA library of Hot
pepper. The subtraction was performed using the PCR-select
cDNA subtraction kit (Clontech, Palo Alto, CA) according
to the manufacturer's instructions. For a faster, cDNA
from HR-developing pepper leaves sampled after 3 days
transcription was synthesized using AMV reverse
pepper leaves was synthesized. After the subtractive
hybridization, the subtracted cDNAs are selectively
amplified by using nested PCR primers to enrich
differentially expressed sequences."

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BASE COUNT      212 a      103 c      118 g      197 t      3 others
ORIGIN
Query Match      97.7%; Score 494.4; DB 14; Length 633;
Best Local Similarity 98.6%; Pred. No. 4.9e-50;
Matches 498; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 1 AAAGAGACTATGCTCGTTCATTACTTCATGAGCATTTCTTGGCAATGACATC 60
DB 74 AAAGAGACTATGCTCGTTCATTACTTCATGAGCATTTCTTGGCAATGACATC 133
QY 61 TTGTGCTTATGGGGTGCAAGCAAGAAITTTGCTGTAAAGAGCTCACAAAACCTGT 120
DB 134 TTGTGCTTATGGGGTGCAAGCAAGAAITTTGCTGTAAAGAGCTCACAAAACCTGT 193
QY 121 AAATGTTCTAGTGAACCTCTATGTCAAAACCTGTATGAGAGAGAAATATGAAGAT 180
DB 194 AAATGTTCTAGTGAACCTCTATGTCAAAACCTGTATGAGAGAGAAATATGAAGAT 253
QY 181 GGTGATTTGTTTCAATCTTAAGCAAGTGTATGATGAGAGATGATGCTAAACT 240
DB 254 GGTGATTTGTTTCAATCTTAAGCAAGTGTATGATGAGAGATGATGCTAAACT 313
QY 241 CTCGCAACAGAAATTTGCTGTGAAGAGAGTCTCTCAAGCAATTAAGTTGATAT 300
DB 314 CTCGCAACAGAAATTTGCTGTGAAGAGAGTCTCTCAAGCAATTAAGTTGATAT 373
QY 301 GGATTTAGTGTACACAAAATTAATAAGTGTGCTCTTAAAGAGGTAACCTTAA 360
DB 374 GGATTTAGTGTACACAAAATTAATAAGTGTGCTCTTAAAGAGGTAACCTTAA 433
QY 361 TGTGATTTCTTGTGTATGATGAGCATTTGACATTAATTAAGTTGTGACATCA 420
DB 434 TGTGATTTCTTGTGTATGATGAGCATTTGACATTAATTAAGTTGTGACATCA 493
QY 421 ATCTTCATGATCTTCTATTAAGTTGTGTGTTTAAAGAAAGAGATCGTTACGCTC 480
DB 494 ATCTTCATGATCTTCTATTAAGTTGTGTGTTTAAAGAAAGAGATCGTTACGCTC 553
QY 481 TAAAAAATTAAGTTGTGTGTTTAAAGAAAGAGATCGTTACGCTC 505
DB 554 TATATGTAAAAAATTAAGTTGTGTGTTTAAAGAAAGAGATCGTTACGCTC 578

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RESULT 2
BM062133      530 bp      mRNA      linear      EST 11-SEP-2002
LOCUS        BM062133
DEFINITION   KS01038H06 KS01 Capsicum annuum cDNA, mRNA sequence.
ACCESSION    BM062133
VERSION      BM062133.1
KEYWORDS     GI:22782251
SOURCE       Capsicum annuum
ORGANISM     Capsicum annuum
            Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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REFERENCE
AUTHORS      Lee S., Kim S.-Y., Chung Y.-H., Shin H.-J., Goh S.-H., Pai H.-S.,
            Hur C.-G. and Choi D.
TITLE        Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
            annuum L.) and Sequence Analysis in Relation to Hypersensitive
            Response Against Pathogen
JOURNAL      Unpublished
COMMENT      Contact: Doil Choi
            Genome Research Center and National Center for Genome Information
            Korea Research Institute of Bioscience and Biotechnology
            P.O. Box 115, Yusong, Taejeon, 305-600, Republic of Korea
            Tel: 82-42-860-4340
            Fax: 82-42-860-4309
            Email: doil@mail.kribb.re.kr
            High quality sequence stop: 530.
FEATURES
SOURCE
            Location/Qualifiers
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            /organism="Capsicum annuum"
            /mol_type="mRNA"
            /cultivar="Bukang"
            /db_xref="taxon:4072"
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            pv. glycines"
            /dev_stage="8 weeks after germination"
            /clone_id="KS01"
            /note="Vector: pBluescript SK(-)"

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BASE COUNT      176 a      76 c      99 g      179 t
ORIGIN
Query Match      96.0%; Score 486; DB 12; Length 530;
Best Local Similarity 98.8%; Pred. No. 5.4e-49;
Matches 500; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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QY 1 AAAGAGACTATGCTCGTTCATTACTTCATGAGCATTTCTTGGCAATGACATC 60
DB 25 AAAGAGACTATGCTCGTTCATTACTTCATGAGCATTTCTTGGCAATGACATC 83
QY 61 TTGTGCTTATGGGGTGCAAGCAAGAAITTTGCTGTAAAGAGCTCACAAAACCTGT 120
DB 84 TTGTGCTTATGGGGTGCAAGCAAGAAITTTGCTGTAAAGAGCTCACAAAACCTGT 143
QY 121 AAATGTTCTAGTGAACCTCTATGTCAAAACCTGTATGAGAGAGAAATATGAAGAT 180
DB 144 AAATGTTCTAGTGAACCTCTATGTCAAAACCTGTATGAGAGAGAAATATGAAGAT 203
QY 181 GGTGATTTGTTTCAATCTTAAGCAAGTGTATGATGAGAGATGATGCTAAACT 240
DB 204 GGTGATTTGTTTCAATCTTAAGCAAGTGTATGATGAGAGATGATGCTAAACT 263
QY 241 CTCGCAACAGAAATTTGCTGTGAAGAGAGTCTCTCAAGCAATTAAGTTGATAT 300
DB 264 CTCGCAACAGAAATTTGCTGTGAAGAGAGTCTCTCAAGCAATTAAGTTGATAT 323
QY 301 GGATTTAGTGTACACAAAATTAATAAGTGTGCTCTTAAAGAGGTAACCTTAA 360
DB 324 GGATTTAGTGTACACAAAATTAATAAGTGTGCTCTTAAAGAGGTAACCTTAA 383
QY 361 TGTGATTTCTTGTGTATGATGAGCATTTGACATTAATTAAGTTGTGACATCA 420
DB 384 TGTGATTTCTTGTGTATGATGAGCATTTGACATTAATTAAGTTGTGACATCA 443
QY 421 ATCTTCATGATCTTCTATTAAGTTGTGTGTTTAAAGAAAGAGATCGTTACGCTC 480
DB 444 ATCTTCATGATCTTCTATTAAGTTGTGTGTTTAAAGAAAGAGATCGTTACGCTC 503
QY 481 TAAAAAATTAAGTTGTGTGTTTAAAGAAAGAGATCGTTACGCTC 506
DB 504 TATATGTAAAAAATTAAGTTGTGTGTTTAAAGAAAGAGATCGTTACGCTC 529

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RESULT 3

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BM064680
 LOCUS BM064680 527 bp mRNA linear EST 11-SEP-2002
 DEFINITION KS01070A06 KS01 Capsicum annuum cDNA, mRNA sequence.
 ACCESSION BM064680
 VERSION BM064680.1 GI:22784798
 KEYWORDS EST.
 SOURCE Capsicum annuum
 ORGANISM Capsicum annuum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Solanales; Capsicum.
 REFERENCE 1 (bases 1 to 527)
 Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pal, H.-S., Hur, C.-G. and Choi, D.
 Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annuum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen
 JOURNAL Unpublished
 COMMENT Contact: Doll Choi
 Genome Research Center and National Center for Genome Information
 Korea Research Institute of Bioscience and Biotechnology
 P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
 Tel: 82-42-860-4340
 Fax: 82-42-860-4309
 Email: doll@mail.krribb.re.kr
 High quality sequence stop: 527.
 Location/Qualifiers
 1..527
 /organism="Capsicum annuum"
 /mol_type="mRNA"
 /cultivar="Bukang"
 /db_xref="taxon:4072"
 /tissue_type="leaf inoculated with Xanthomonas campestris pv. glycines"
 /dev_stage="8 weeks after germination"
 /clone_lib="KS01"
 /note="Vector: pBluescript SK(-)"

BASE COUNT 175 a 74 c 100 g 178 t
 ORIGIN
 Query Match 90.7%; Score 459; DB 12; Length 527;
 Best Local Similarity 96.7%; Pred. No. 8.7e-46;
 Matches 492; Conservative 0; Mismatches 10; Indels 7; Gaps 2;

QY 1 AAAGACTATGCGCTGCTTCACTTCAATGACGATTTCTGTCGCAATGACATC 60
 DB 22 AAAGACTATGCGCTGCTTCACTTCAATGACGATTTCTGTCGCAATGACATC 81
 QY 61 TTGTGCTTATGGGGTGCAGCAAGAAATTTGCTGAAGAGCTCAAAAACCTGTT 120
 DB 82 TTGTGCTTATGGGGTGCAGCAAGAAATTTGCTGAAGAGCTCAAAAACCTGTT 141
 QY 121 AAATGTTCTAGTACCTCTATGTCAAAACCTGATGAGAGAGAGAAATATGAGAT 180
 DB 142 AAATGTTCTAGTACCTCTATGTCAAAACCTGATGAGAGAGAGAAATATGAGAT 201
 QY 161 GGTCTATGTTTACAACTCTAGCAAGAGCTTATGATGATGATGATGATGATGAT 240
 DB 202 GGTCTATGTTTACAACTCTAGCAAGAGCTTATGATGATGATGATGATGATGAT 261
 QY 241 CTCGCAACGAATGCTGCTGGAAGAGAGTTCCTCAAGAGAGTATTAAGTTGATAT 300
 DB 262 CTCGCAACGAATGCTGCTGGAAGAGAGTTCCTCAAGAGAGTATTAAGTTGATAT 318
 QY 301 GGATTTAGTGCACAAAAT-----TAAATAAAGGTTTCTTTCTTAAAGGTAAT 356
 DB 319 GGATTTAGTGCACAAAATTAATAAAGGTTTCTTTCTTAAAGGTAAT 378
 QY 357 ATAATGTTGATTTCTGTTGATAGTATGACATTTGACATTAATTAAGTTGACAC 416
 DB 379 ATAATGTTGTTCTTCTGTTGATAGTATGACATTTGACATTAATTAAGTTGACAC 438
 QY 417 ATCAATCCTTATGATATCTTATTAAGTTGTTGTTTATGAAGAGATCGTTAC 476

DB 439 ATCAATCCTTATGATATCTTATTAAGTTGTTGTTTATGAAGAGATCGTTAC 498
 QY 477 GGCTTAAAAA
 DB 499 GGCTTATATGTAATAAAAAAAAAAAAAA 527

RESULT 4
 CB185066 648 bp mRNA linear EST 03-FEB-2003
 LOCUS KS04236T70 KS04 Capsicum chinense cDNA, mRNA sequence.
 DEFINITION CB185066
 ACCESSION CB185066
 VERSION CB185066.1 GI:28197059
 KEYWORDS EST.
 SOURCE Capsicum chinense
 ORGANISM Capsicum chinense
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Solanales; Capsicum.
 REFERENCE 1 (bases 1 to 648)
 Lee, S.-J., Lee, M.-Y., Choi, S.-H., Her, N.-H., Yang, S.-G. and Harn, C.-H.
 Generation of Expressed Sequence Tags from Hot Pepper (Capsicum chinense) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen
 JOURNAL Unpublished
 COMMENT Contact: Chee Hark Harn
 Biotechnology center
 NONG WO BIO CO., LTD.
 537-17 Jeongdan, Ganam, Yeosu, Jeonnam, 550-705, Republic of Korea
 Tel: 82 31 883 7055
 Fax: 82 31 884 7065
 Email: chharn@nongwoobio.co.kr
 Seq primer: 77.
 Location/Qualifiers
 1..648
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 /mol_type="mRNA"
 /cultivar="P1257284"
 /db_xref="taxon:80379"
 /sex="hermaphrodite"
 /tissue_type="leaf"
 /dev_stage="7-8 weeks-old leaves"
 /clone_lib="KS04"
 /note="Vector: pGEM-T easy; Site 1: EcoRI; PMV-induced suppression subtractive cDNA library of Hot pepper. The subtraction was performed using the PCR-select cDNA subtraction kit (Clontech, Palo Alto, CA) according to the manufacturer's instructions. For a tester, cDNA from HR-developing pepper leaves sampled after 3 days inoculation was synthesized using AMV reverse transcriptase while, for a driver, cDNA from noninoculated pepper leaves was synthesized. After the subtractive hybridization, the subtracted cDNAs are selectively amplified by using nested PCR primers to enrich differentially expressed sequences."

BASE COUNT 197 a 115 c 132 g 196 t
 ORIGIN
 Query Match 87.6%; Score 443.2; DB 14; Length 648;
 Best Local Similarity 93.1%; Pred. No. 5.8e-44;
 Matches 471; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 1 AAAGACTATGCGCTGCTTCACTTCAATGACGATTTCTGTCGCAATGACATC 60
 DB 123 AAAGACTATGCGCTGCTTCACTTCAATGACGATTTCTGTCGCAATGACATC 182
 QY 61 TTGTGCTTATGGGGTGCAGCAAGAAATTTGCTGAAGAGCTCAAAAACCTGTT 120
 DB 183 TTGTGCTTATGGGGTGCAGCAAGAAATTTGCTGAAGAGCTCAAAAACCTGTT 242
 QY 121 AAATGTTCTAGTACCTCTATGTCAAAACCTGATGAGAGAGAGAAATATGAGAT 180

RESULT 5	LOCUS	DEFINITION
CB164889	CB164889	506 bp mRNA linear EST 30-JAN-2003
CB164889	KS05014370	KS05 Capsicum annuum cDNA, mRNA sequence.

Email: chharn@nongwoobio.co.kr
Seq primer: T7.

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1... 506
/organism="Capeicum annum"
/mol_type="mRNA"
/cultivar="SFO, SBV"
/db_xref="taxon:4072"
/sex="hermaphrodite"
/tissue_type="fruit"
/dev_stage="mature red"
/clone_id="K805"
/note="Vector: pGEM-T easy; Site1: EcoRI, SfoI red - SBV
red suppression subtractive cDNA library of hot pepper.
The subtraction was performed using the PCR-select cDNA
subtraction kit (Clontech, Palo Alto, CA) according to the
manufacturer's instructions. For a tester, cDNA from
HR-developing pepper leaves sampled after 3 days
inoculation was synthesized using AMV reverse
transcriptase while, for a driver, cDNA from noninoculated
pepper leaves was synthesized. After the subtractive
hybridization, the subtracted cDNAs are selectively
amplified by using nested PCR primers to enrich
differentially expressed sequences."

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/db_xref="raxon:4072"
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/tissue_type="fruit"
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/clone.lib="KS05"
 /note="Vector: pGEM-T easy; Site 1: EcoRI; SRO red - SBV
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 The subtraction was performed using the PCR-select cDNA
 subtraction kit (Clontech, Palo Alto, CA) according to the
 manufacturer's instructions. For a tester, cDNA from
 HR-developing pepper leaves sampled after 3 days
 inoculation was synthesized using AMV reverse
 transcriptase while, for a driver, cDNA from noninoculated
 pepper leaves was synthesized. After the subtractive
 hybridization, the subtracted cDNAs are selectively
 amplified by using nested PCR primers to enrich
 differentially expressed sequences."

BASE COUNT
 ORIGIN

Query Match 83.2%; Score 421; DB 14; Length 496;
 Best Local Similarity 97.7%; Pred. No. 2.9e-41;
 Matches 427; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 AAAGAGCTATGCGCTGCTTCCATTTCTTATGAGCATTTCTTGGCAATGACATC 60
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 QY 61 TTGTTGCTTATGCGGTCGAAGCAAGAAATTTGCTGTAAGAGCTCACAAAACCTGTT 120
 DB 120 TTGTTGCTTATGCGGTCGAAGCAAGAAATTTGCTGTAAGAGCTCACAAAACCTGTT 179
 QY 121 AAATGTTCTAGTACCTCTATGCAAAAACCTCTATGAGAGAGAAATATGAGAT 180
 DB 180 AAATGTTCTAGTACCTCTATGCAAAAACCTCTATGAGAGAGAAATATGAGAT 239
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 DB 240 GGTCTTTGTTTACAACTCTTAAGCAAGTCTTATGCAAGAGATGTAATGCTTAAACT 299
 QY 241 CTCGCAACGAAATGCTTGAAGAGAGTCTTCAAGCAAGTAAATTAAGTTGATAT 300
 DB 300 CTCGCAACGAAATGCTTGAAGAGAGTCTTCAAGCAAGTAAATTAAGTTGATAT 359
 QY 301 GGATTTAGTGCACAAAATTAATAAAGTGTGCTTTCTTAAAGGTAACCTTAA 360
 DB 360 GGATTTAGTGCACAAAATTAATAAAGTGTGCTTTCTTAAAGGTAACCTTAA 419
 QY 361 TGTGTATTTCTGCTGTATAGGCAATTTGACATTAATAAGTTGTACACATCA 420
 DB 420 TGTGTATTTCTGCTGTATAGGCAATTTGACATTAATAAGTTGTACACATCA 479
 QY 421 ATCCTTCATGTATCTTC 437
 DB 480 TTCCTTCATGTATCTTC 496

RESULT 7
 LOCUS BM063527 540 bp mRNA linear EST 11-SEP-2002
 DEFINITION KS01056D12 KS01 Capsicum annuum cDNA, mRNA sequence.
 ACCESSION BM063527
 VERSION BM063527.1 GI:22783645
 KEYWORDS EST.
 SOURCE Capsicum annuum
 ORGANISM Capsicum annuum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Solanales; Solanaceae; Capsicum.
 REFERENCE 1 (bases 1 to 540)
 Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-U., Goh, S.-H., Pal, H.-S.,
 Hur, C.-G. and Choi, D. Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
 annuum L.) and Sequence Analysis in Relation to Hypersensitive
 Response Against Pathogen
 JOURNAL Unpublished
 COMMENT Contact: Doll Choi

Genome Research Center and National Center for Genome Information
 Korea Research Institute of Bioscience and Biotechnology
 P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
 Tel.: 82-42-860-4340
 Fax: 82-42-860-4309
 Email: doll@mail.krdb.re.kr
 High quality sequence stop: 540.
 Location/Qualifiers
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 /organism="Capsicum annuum"
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 /db_xref="taxon:4072"
 /issue_type="leaf inoculated with Xanthomonas campestris
 pv. glycines"
 /dev_stage="8 weeks after germination"
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 /note="Vector: pBluescript SK(-)"

BASE COUNT 185 a 77 c 103 g 175 t

Query Match 74.7%; Score 378; DB 12; Length 540;
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 Matches 454; Conservative 0; Mismatches 45; Indels 19; Gaps 3;

QY 1 AAAGAGCTATGCGCTGCTTCCATTTCTTATGAGCATTTCTTGGCAATGACATC 60
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 QY 61 TTGTTGCTTATGCGGTCGAAGCAAGAAATTTGCTGTAAGAGCTCACAAAACCTGTT 120
 DB 90 TTGTTGCTTATGCGGTCGAAGCAAGAAATTTGCTGTAAGAGCTCACAAAACCTGTT 149
 QY 121 AAATGTTCTAGTACCTCTATGCAAAAACCTCTATGAGAGAGAAATATGAGAT 180
 DB 150 AAATGTTCTAGTACCTCTATGCAAAAACCTCTATGAGAGAGAAATATGAGAT 209
 QY 181 GGTCTTTGTTTACAACTCTTAAGCAAGTCTTATGCAAGAGATGTAATGCTTAAACT 229
 DB 210 GGTCTTTGTTTACAACTCTTAAGCAAGTCTTATGCAAGAGATGTAATGCTTAAACT 269
 QY 230 ATGCTAAACTCTGCAACGAAATGCTTGAAGAGAGTCTTCAAGCAAGTAAAT 288
 DB 270 ATGCTAAACTCTGCAACGAAATGCTTGAAGAGAGTCTTCAAGCAAGTAAAT 329
 QY 289 AAGTTGATTTGATTTAGTGTACACAAAATTAATAAAGTGTGCTTTCTTAAAG 348
 DB 330 AAGTTGATTTGATTTAGTGTACACAAAATTAATAAAGTGTGCTTTCTTAAAG 389
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 DB 390 GGTAACTTAATATGTTGATCTGCTGTATAGGCAATTTGACATTAATAAGT 448
 QY 409 TGTGACATCAATCTTCATGTATCTTCTTAAAGTTGTGCTTTTAAATGAAGAAGA 468
 DB 449 TGTGACATCAATCTTCATGTATCTTCTTAAAGTTGTGCTTTTAAATGAAGAAGA 502
 QY 469 TCGTTTACGTCATAAAAAAAAAAAAAAAAAAAAAA 506
 DB 503 TCGTTTACGTCATAAAAAAAAAAAAAAAAAAAAAA 540

RESULT 8
 LOCUS BM065064 580 bp mRNA linear EST 11-SEP-2002
 DEFINITION KS01074E11 KS01 Capsicum annuum cDNA, mRNA sequence.
 ACCESSION BM065064
 VERSION BM065064.1 GI:22785182
 KEYWORDS EST.
 SOURCE Capsicum annuum
 ORGANISM Capsicum annuum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 580)	Lee, S.-Y., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pal, H.-S., Hur, C.-G., and Choi, D.	Generation of Expressed Sequence Tags from Hot Pepper (<i>Capsicum annuum</i> L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen	Unpublished	
	Contact: Doil Choi			
	Genome Research Center and National Center for Genome Information			
	Korea Research Institute of Bioscience and Biotechnology			
	P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea			
	Tel: 82-42-860-4340			
	Fax: 82-42-860-4309			
	Email: doil@mail.krdb.re.kr			
	High quality sequence stop: 580.			
	Location/Qualifiers			
	1. 580			
	/organism="Capsicum annuum"			
	/mol_type="mRNA"			
	/cultivar="Bukang"			
	/db_xref="taxon:4072"			
	/tissue_type="leaf inoculated with <i>Xanthomonas campestris</i> pv. <i>glycinis</i> "			
	/dev_stage="8 weeks after germination"			
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Best Local Similarity	87.5%;	Pred. 5.3e-36;		
Matches 453;	Conservative 0;	Mismatches 46;	Indels 19;	Gaps 3;
OY	1	AAAGAGACTATGGCTCGTTCACATTTACTCATGAGGACATTTCTGTCTGGCANTGACATC	60	
DB	28	AATGAGCATTAAGGCTCGTTCACATTTACTCATGAGGACATTTCTGTCTGGCANTGACATC	87	
OY	61	TTTGTGCTTATGGGGTGCAGGCAAGAAATTTGCTGAAGAGCTCACAACCTGTT	120	
DB	88	TTTGTGCGCAATGAGGTGCAGAGTAAAGAAATTTGCTGAAGAGTCTCAGACCTGTT	147	
OY	121	AAATGCTTACAGACCCCTATATGCATAAAACCTCTATAGAGAGAAATATGAAGT	180	
DB	148	ATATGTTCTAGACCCCGCTATGTCAACAAATCTGATTTAAAGAGAGAACTATGAAGT	207	
OY	181	GGTCATTTTTCACATCCTTAAGCAAGGCTTATGCATGAAGAGATGA-----	229	
DB	208	GGTATTTGTTCAACATCCTTAAGCAAGGCTTATGCATGAAGAGATGA-----	267	
OY	230	ATGCTAAACCTCTGCACACAGAAATTCCTGCTTGAAGAGAGTTCCTCAGACAGTAAT	288	
DB	268	GATGTAAACCTCTGCACACAGAAATTCCTGCTTGAAGAGAGTTCCTCAGACAGTAAT	327	
OY	289	AAGTTGATTTATGATTTATAGTGCACACAAATTTAAATAAAGTGTGCTTTCTTAAAG	348	
DB	328	AAAGTTGATTTATGATTTATAGTGCACACAAATTTAAATAAAGTGTGCTTTCTTAAAG	387	
OY	349	GGTAACTTATAATGTTGTAATTTCTTGATATGAGCCATTTGACACATTAATTTAAAGT	408	
DB	388	GGTAACTTATAATGTTGTTCTTGATATGAGCCATTTGACACATTAATTTAAAGT	446	
OY	409	TGTGACATCATCCTTCATGATCTTCTATTAAGTTTGTGTTTAAAGAAAGAGA	468	
DB	447	TGTGACATCATCCTTCATGATCAACTT-----TGTGTTCTTTTAAATGAAAGAGA	500	
OY	469	TGTTTACGTTCTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT	506	
DB	501	TGTTTACGTTCTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT	538	

LOCUS	CB185076	720 bp	mRNA	linear	EST 03-FEB-2003
DEFINITION	KS04192710 KS04 Capsicum chinense cDNA, mRNA sequence.				
ACCESSION	CB185076				
VERSION	CB185076.1	GI:28197069			
KEYWORDS	EST.				
SOURCE	Capsicum chinense				
ORGANISM	Capsicum chinense				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Capsicum.				
AUTHORS	1 (bases 1 to 720) Lee,S.-J., Lee,M.-Y., Choi,S.H., Her,N.H., Yang,S.G. and Harn,C.H.				
TITLE	Generation of Expressed Sequence Tags from Hot pepper(Capsicum chinense) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen				
JOURNAL	Unpublished				
COMMENT	Contact: Chee Hark Harn Biotechnology center NONG WO0 BIO CO.,LTD. 537-17 Jeongdan, Ganam, Yeosu, Kyonggi 469-885, Republic of Korea Tel: 82 31 883 7055 Fax: 82 31 884 7065 Email: chharn@nongwoobio.co.kr Seq primer: 77				
FEATURES	Location/Qualifiers				
source	1..720 /organism="Capsicum chinense" /mol_type="mRNA" /culivar="PI257284" /db_xref="taxon:80379" /sex="hermaprodite" /tissue_type="leaf" /dev_stage="7-8 weeks-old leaves" /clone_id="KS04" /note="Vector: pGEM-T easy; Site 1: EcoRI; PMW-induced suppression subtractive cDNA library of Hot pepper. The subtraction was performed using the PCR-select cDNA subtraction kit (Clontech, Palo Alto, CA) according to the manufacturer's instructions. For a tester, cDNA from HR-developing pepper leaves sampled after 3 days inoculation was synthesized using AMV reverse transcriptase while, for a driver, cDNA from noninoculated pepper leaves was synthesized. After the subtractive hybridization, the subtracted cDNAs are selectively amplified by using nested PCR primers to enrich differentially expressed sequences."				
BASE COUNT	203 a 114 c 133 g 218 t 52 others				
ORIGIN					
	Query Match 73.6%; Score 372.2; DB 14; Length 720; Best Local Similarity 90.5%; Pred. No.1.5e-35; Matches 431; Conservative 0; Mismatches 37; Indels 8; Gaps 4;				
1	AAAGAGCTATGGCTGCTTCATTTCTTGTGCGCAATGACACTC 60				
191	AAAGAGCTATGGCTGCTTCATTTCTTGTGCGCAATGACACTC 250				
61	TTTGTGCTTATGGGAGTGCAGGCAAGAAATTTGCTGTAAAGACTCAGAAAACCTGTT 120				
251	TTTGTGCTTATGGGAGTGCAGGCAAGAAATTTGCTGTAAAGACTCAGAAAACCTGTT 310				
121	AAATGCTCTAGTACCTCTATGCAAAAACCTGTATGAGAGGAAATATGAAGAT 180				
311	AAATGCTCTAGTACCTCTATGCAAAAACCTGTATGAGAGGAAATATGAAGAT 370				
181	GGTGATTTGTTCACAATCTTAAGCAAGTGTATGATGAAGAGATTAATGCTAAACT 240				
371	GGTGATTTGTTCACAATCTTAAGCAAGTGTATGATGAAGAGATTAATGCTAAACT 430				
241	CTGGCAACAGAAATGCT-TCCTTGAAGAGAGTTCTCAAGCAAGTAAATTAAGTTGATTA 299				
431	CTGGCAACAGAAATGCTTCTTGAAGAGAGTTCTCAAGCAAGTAAATTAAGTTGATTA 490				

QY 300 TGGATTAGTGCACACAAATTAATAAGTGTGCTTCTTAAAA--GGGTAACTTA 357
 DB 491 TGGATTAGTGCACACAAATTAATAAGTGTGCTTCTTAAAAAGGGGTAACTTA 550
 QY 358 TAATGTTGTAATCTTGGTGA-TAGTAGCATTTGACACATTAATAAGTTGACAC 416
 DB 551 TAAGTTGTAATCTTNGAANAATAGTGCATTTGACACATTAATAAGTTGAGNAC 610
 QY 417 ATCAAT---CCTTATGATCTTCTTAAATTTGTGTGTTTATGAAAAAGAA 468
 DB 611 AACTTAATCCCTTAAATGTTCTTAAATGTTGAGNACATTAAGTAAAAANA 666
 RESULT 10
 CA525505 545 bp mRNA linear EST 15-NOV-2002
 LOCUS CA525505
 DEFINITION KS12056G07 KS12 Capsicum annum cDNA, mRNA sequence.
 ACCESSION CA525505
 VERSION CA525505.1 GI:25039585
 KEYWORDS EST
 SOURCE Capsicum annum
 ORGANISM Capsicum annum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Solanales; Solanaceae; Capsicum.
 1 (bases 1 to 545)
 Lee,S., Kim,S.-Y., Chung,Y.-H., Shin,H.-J., Goh,S.-H., Pai,H.-S.,
 Hur,C.-G. and Choi,D.
 Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
 annum L.) and Sequence Analysis in Relation to Hypersensitive
 Response Against Pathogen
 Unpublished
 JOURNAL Contact: Doil Choi
 COMMENT Genome Research Center and National Center for Genome Information
 Korea Research Institute of Bioscience and Biotechnology
 P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
 Tel: 82-42-860-4340
 Fax: 82-42-860-4309
 Email: doil@mail.krdb.re.kr
 Plate: 056 row: G column: 07.
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:4072"
 /clone_lib="KS12"
 BASE COUNT 182 a 84 c 106 g 173 t
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 Query Match 71.9%; Score 364; DB 14; Length 545;
 Best Local Similarity 86.5%; Pred. No. 1,6e-34; Indels 19; Gaps 3;
 Matches 443; Conservative 0; Mismatches 50;
 QY 1 AAAGAGCTATGGCTGCTTCATTTACTTCATGAGCATTTCTTGGCAATGACATC 60
 DB 41 AAAGTACTATGGCTGCTTCATTTACTTCATGAGCATTTCTTGGCAATGACATC 100
 QY 61 TTTGTTGCTTATGGGTGCAAGCAAGAAATTTGCTGTAAGAGCTCAAAAACCTGTT 120
 DB 101 TTTGTTGCCAATGAGGTGCAAGGTAAAGAAATTTGCTGTAAGATGTCACAGAGCTGTT 160
 QY 121 AAATGTTCTAGTACACCTCTATGTCAAAAACCTGTATGAGAAGAAATATGAAGT 180
 DB 161 AATATGTTCTAGTACACCTCTATGTCAAAAACCTGTATGAGAAGAAATATGAAGT 220
 QY 181 GGTATGTTCTTCAATCTTAAGCAAGTCTTATGATGATGAAGAGATGTA----- 229
 DB 221 GGTATGTTCTTCAATCTTAAGCAAGTCTTATGATGATGAAGAGATGTAAGTCTTCA 280
 QY 230 -ATGCTAAACCTCTGCAACAGAAATGCTTCTTGAAGAAAGTCTCTCAAGCATTAAT 288
 DB 281 GATGTTAAACCTCTGCAACAGAAATGCTTCTTGAAGAAAGTCTCTCAAGCATTAAT 340

QY 289 AAGTTGATATGATTAAGTATGTCACACAAATTAATAAGTGTGCTTCTTAAAAAG 348
 DB 341 AAGTTGATATGATTAAGTATGTCACACAAATTAATAAGTGTGCTTCTTAAAAAG 400
 QY 349 GGTAACTTATATGTTGATTTCTTGGTATAGTACCATTTGACACATTAATAAGT 408
 DB 401 GGTAACTTATATGTTGATTTCTTGGTATAGTACCATTTGACACATTAATAAGT 459
 QY 409 TGTACACATTAATCTTCAATGATCTTCTATTAAGTTGTGTTTTTAATGAAGAAG 468
 DB 460 TGTACACATTAATCTTCAATGATCTTCTATTAAGTTGTGTTTTTAATGAAGAAG 513
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 RESULT 11
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 LOCUS BM063616
 DEFINITION KS01057E08 KS01 Capsicum annum cDNA, mRNA sequence.
 ACCESSION BM063616
 VERSION BM063616.1 GI:22783734
 KEYWORDS EST
 SOURCE Capsicum annum
 ORGANISM Capsicum annum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Solanales; Solanaceae; Capsicum.
 1 (bases 1 to 448)
 Lee,S., Kim,S.-Y., Chung,Y.-H., Shin,H.-J., Goh,S.-H., Pai,H.-S.,
 Hur,C.-G. and Choi,D.
 Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
 annum L.) and Sequence Analysis in Relation to Hypersensitive
 Response Against Pathogen
 Unpublished
 JOURNAL Contact: Doil Choi
 COMMENT Genome Research Center and National Center for Genome Information
 Korea Research Institute of Bioscience and Biotechnology
 P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
 Tel: 82-42-860-4340
 Fax: 82-42-860-4309
 Email: doil@mail.krdb.re.kr
 High quality sequence stop: 448.
 Location/Qualifiers
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 /organism="Capsicum annum"
 /mol_type="mRNA"
 /cultivar="Bukang"
 /db_xref="taxon:4072"
 /tissue_type="leaf inoculated with Xanthomonas campestris
 pv. glycines"
 /dev_stage="8 weeks after germination"
 /clone_lib="KS01"
 /note="Vector: pBluescript SK(-)"
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 Query Match 71.9%; Score 363.8; DB 12; Length 448;
 Best Local Similarity 99.5%; Pred. No. 2e-34; Indels 2; Gaps 0;
 Matches 365; Conservative 0; Mismatches 2;
 QY 1 AAAGAGCTATGGCTGCTTCATTTACTTCATGAGCATTTCTTGGCAATGACATC 60
 DB 45 AAAGAGCTATGGCTGCTTCATTTACTTCATGAGCATTTCTTGGCAATGACATC 104
 QY 61 TTTGTTGCTTATGGGTGCAAGCAAGAAATTTGCTGTAAGAGCTCAAAAACCTGTT 120
 DB 105 TTTGTTGCTTATGGGTGCAAGCAAGAAATTTGCTGTAAGAGCTCAAAAACCTGTT 164
 QY 121 AAATGTTCTAGTACACCTCTATGTCAAAAACCTGTATGAGAAGAAATATGAAGT 180
 DB 165 AAATGTTCTAGTACACCTCTATGTCAAAAACCTGTATGAGAAGAAATATGAAGT 224

QY	181	GGTCAATGTTTTCACAAATCCTTAAGCAAGGCTTAATGCAGAAAGATGTAATCTAAACT	240
Db	225	GGTCAATGTTTTCACAAATCCTTAAGCAAGGCTTAATGCAGAAAGATGTAATCTAAACT	284
QY	241	CTCGCAACAGAAATGCTGCTTGAAGAGAGTTCTCAAGCAGTAATTAAGTTGATTAAT	300
Db	285	CTCGCAACAGAAATGCTGCTTGAAGAGAGTTCTCAAGCAGTAATTAAGTTGATTAAT	344
QY	301	GGATTAGTGTCACACAAATAATTAATGAAGTGTGCTTTCTTAAGAAGGTAACTATTA	360
Db	345	GGATTAGTGTCACACAAATAATTAATGAAGTGTGCTTTCTTAAGAAGGTAACTATTA	404
QY	361	TGTTGTA 367	
Db	405	TGTTGTA 411	
RESULT 12			
LOCUS	BM062737	535 bp	mRNA linear EST 11-SEP-2002
DEFINITION	KS01046F09 KS01 Capsicum annuum cDNA, mRNA sequence.		
VERSION	BM062737.1	GI:22782855	
KEYWORDS	EST.		
SOURCE	Capsicum annuum		
ORGANISM	Capsicum annuum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; Lamiales; Solanales; Solanaceae; Capsicum.		
AUTHORS	Lee,S.-Y., Kim,S.-Y., Chung,Y.-H., Shin,H.-J., Goh,S.-H., Pai,H.-S., Hur,C.-G. and Choi,D.		
TITLE	Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annuum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen		
JOURNAL	Unpublished		
COMMENT	Contact: Doil Choi Genome Research Center and National Center for Genome Information Korea Research Institute of Bioscience and Biotechnology P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea Tel: 82-42-860-4340 Fax: 82-42-860-4309 Email: doil@email.kribb.re.kr High quality sequence step: 535. Location/Qualifiers 1..535 /organism="Capsicum annuum" /mol_type="mRNA" /cultivar="Bukang" /db_xref="taxon:4072" /tissue.type="leaf inoculated with Xanthomonas campestris pv. glycines" /dev_stage="8 weeks after germination" /clone_lib="KS01" /note="vector: pBluescript SK(-)"		
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BASE COUNT	172 a 80 c 106 g 177 t		
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Query Match:	71.9%;	Score 363.6;	DB 12
Best Local Similarity	85.9%;	Pred. No. 1.8e-34;	Length 535;
Matches 445;	Conservative 0;	Mismatches 54;	Indels 19; Gaps 3
QY	1	AAAGAGCATAGGCTGCTTCATTTACTTCATGCGCATTTCTTGCTTGCGCAATGACATC	60
Db	24	AAAGAGCATAGGCTGCTTCATTTACTTCATGCGCATTTCTTGCTTGCGCAATGACATC	83
QY	61	TTTGTGCTATGGGGTGCAGGCAAGAAATTTGCTGTAAAGACTACAAAACCTGTT	120
Db	84	TTTGTGCTATGGGGTGCAGGCAAGAAATTTGCTGTAAAGATGTCACAGACTGTT	143
QY	121	AAATGTTTAGAGACCTCTATGTCAAAAACCTGTATGGAAGAAGAAATATGAAGT	180

Db	144	ATATGTTCTAGTGCACCCGGCATGTAAACAATCTGTATCGAAGAGCAAACTATGAAGAT	203
Oy	181	GCTAATTGTTTCACAAATCCTTAAGAAGTGCTTAGCATGAAAGATACTA-----	229
Db	204	GGTATATTGTTTACAAATCTCTTAAGGAAGGCGTATGATGATGAGAAATGATATGTGGTTTCAG	263
Oy	230	-ATGCTAAAACCTCTCGAACAGAAATTCCTGCTTGAAGAGAGTTCCTCAAGCAGTAAT	288
Db	264	GATGTTAAATCTCTCGACGAAAAATTCGTTCTGAAAAAGAGTTTCTCAAGCAGTAAT	323
Oy	289	AAGTTTGATTAATGGAATTTAGTGTACACCAAATTAATTAAGTGTGCTTTCTTAAAG	348
Db	324	AAGTTTGATTAATGGAATTTAGTGTACACCAAATTAATTAAGTGTGCTTTCTTAAAG	383
Oy	349	GSTACTATTAATGTGTGATTTCTTGSGTATAGTAGGCAATTTGACACATTAATTAAGT	408
Db	384	GSTACTATTAATGTGTGATTTCTTGSGTATAGTAGGCAATTTGACACATTAATTAAGT	442
Oy	409	TGTGACACATCAATCTCTTCATGTATCTTCTTATTAAGTTTGTGTCTTTTAAAGAAAGA	468
Db	443	TGTGACACATCAATCTCTTCATGTATCTTCTTATTAAGTTTGTGTCTTTTAAAGAAAGA	496
Oy	469	TCGTTTACGCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	506
Db	497	TCGTTTACGATCAATGTATGTATGAAAAAAAAAAAAAAAAA	534
RESULT 13	CAS15866	571 bp	mRNA linear EST 15-NOV-2002
LOCUS	KS09048BE1	KS09 Capsicum annuum cDNA, mRNA sequence.	
DEFINITION	CAS15866		
ACCESSION	CAS15866.1	GI:25016423	
KEYWORDS	EST.		
SOURCE	Capsicum annuum		
ORGANISM	Capsicum annuum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Capsicum.		
AUTHORS	Lee,S., Kim,S.-Y., Chung,Y.-H., Shin,H.-J., Goh,S.-H., Pai,H.-S., Hur,C.-G. and Choi,D.		
TITLE	Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annuum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen		
JOURNAL COMMENT	Contact: Dool Choi Genome Research Center and National Center for Genome Information Korea Research Institute of Bioscience and Biotechnology P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea Tel.: 82-42-860-4340 Fax: 82-42-860-4309 Email: doilemail.kr@db.re.kr Plate: 048 row: E column: 11.		
FEATURES	Location/Qualifiers		
SOURCE	1..571		
BASE COUNT	202 a 90 c 95 g 184 t		
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Query Match	Best Local Similarity 71.1%; Score 360; DB 14; Length 571;		
Matches	453; Conservative 0; Mismatches 45; Indels 16; Gaps 5;		
Oy	1	AAAGAGCATATGCTCGTTCATTACTTACATGCGATTTCTTGCTTGGCAATATACACTC	60
Db	46	AAAGAGATTAATGCTCGTTCATTACTTACATGCGATTTCTTGCTTGGCAATATACACTC	105
Oy	61	TTTGTGCTTATGGGGGCAAGGCAAGAAATTTGCTGTAAGAGCTCACAAACCTGTT	120

Db 106 TTGTGGCTATGGGGTCAAGTAAAGAAATTCCTGTAAAGTCCCAACACCTTT 165
 Qy 121 AATGTTCTAGTACCCCTCTATGTCAAAAACCTCTGTATGAGAGAGAAATATGAAT 180
 Db 166 CTATGTACTAAAGACCTTCATAGCAAGACACTCTGT---TCCAGGTAACTATGAAT 222
 Qy 181 GGTCAATGTTTCAACATCTTAAGCAAGTCTTATGATGAAGATGT-----AATGT 234
 Db 223 GGTCAATGTTTCAACATCTTATGATGAAGTCTTATGATGAAGATGT 282
 Qy 235 AAACTCTCGCAACGAATTCCTGCTTGAAGAGATTCCTCAAGCATTAATTAAGTT 294
 Db 283 AAAAAGCTCGACAGGAA---TTGCTGAAGAGAGTTTCTCAAGCATTAATTAATTT 338
 Qy 295 GATTATGATTTAGTGTACACAAAATTAATTAAGTGTGCTTTCTTAAAGGTTAC 354
 Db 339 AATTATGATTTAGTGTACACAAAATTAATTAAGTGTGCTTTCTTAAAGGTTAC 398
 Qy 355 TTATATGATTTAGTGTACACAAAATTAATTAAGTGTGCTTTCTTAAAGGTTAC 414
 Db 399 TTATATGATTTAGTGTCTTGACATATAGTACCATTTGACATTAATTAAGTGTGAC 457
 Qy 415 ACATCAATCTTCAATGATCTTCTTATTAAGTGTGCTTTCTTAAAGGATCGT 472
 Db 458 ACATCAATCTTCAATGATCTTCTTATTAAGTGTGCTTTCTTAAAGGATCGT 517
 Qy 473 TTACGCTCTAAATAAAAAAAAAAAAAAAAAAAAAA 506
 Db 518 TTACGCTCTAAATAAAAAAAAAAAAAAAAAAAAAA 551

RESULT 14
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 LOCUS KS01068D09 KS01 Capsicum annuum cDNA, mRNA sequence.
 DEFINITION BM064540
 ACCESSION BM064540.1 GI:22784658
 VERSION EST
 KEYWORDS

SOURCE Capsicum annuum
 ORGANISM Capsicum annuum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Solanales; Solanaceae; Capsicum.

REFERENCE 1 (bases 1 to 537)
 Lee,S., Kim,S.-Y., Chung,Y.-H., Shin,H.-J., Goh,S.-H., Pai,H.-S.,
 Hur,C.-G. and Choi,D.
 Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
 annuum L.) and Sequence Analysis in Relation to Hypersensitive
 Response Against Pathogen

TITLE Unpublished
 JOURNAL Contact: Doil Choi
 COMMENT Genome Research Center and National Center for Genome Information
 Korea Research Institute of Bioscience and Biotechnology
 P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
 Tel: 82-42-860-4340
 Fax: 82-42-860-4309
 Email: doil@mail.kribb.re.kr
 High quality sequence stop: 537.

FEATURES
 source
 1. 537
 Location/Qualifiers
 /organism="Capsicum annuum"
 /mol_type="mRNA"
 /cultivar="Bukang"
 /db_xref="taxon:4072"
 /rname_type="leaf inoculated with Xanthomonas campestris
 pv. glycines"
 /dev_stage="8 weeks after germination"
 /clone_id="KS01"
 /notes="Vector: pBluescript SK(-)"

BASE COUNT 176 a 83 c 97 g 181 t
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 Query Match 70.5%; Score 356.8; DB 12; Length 537;

Best Local Similarity 87.7%; Pred. No. 1,26-33;
 Matches 451; Conservative 0; Mismatches 47; Indels 16; Gaps 5;

Qy 1 AAAGACTATAGCTCGTTCATTACTTCATGCAATTTCTTGTGGCAATGACATC 60
 Db 30 AAAAGACTATAGCTCGTTCATTACTTCATGCAATTTCTTGTGGCAATGACATC 89
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 Qy 121 AATGTTCTAGTACCCCTCTATGTCAAAAACCTGTATGAGAGAAATATGAAGAT 180
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 Qy 295 GATTATGATTTAGTGTACACAAAATTAATTAAGTGTGCTTTCTTAAAGGTTAC 354
 Db 323 AATTATGATTTAGTGTACACAAAATTAATTAAGTGTGCTTTCTTAAAGGTTAC 382
 Qy 355 TTATATGATTTAGTGTCTTGATATAGTACCATTTGACATTAATTAAGTGTGAC 414
 Db 383 TTATATGATTTAGTGTCTTGATATAGTACCATTTGACATTAATTAAGTGTGAC 441
 Qy 415 ACATCAATCTTCAATGATCTTCTTATTAAGTGTGCTTTCTTAAAGGATCGT 472
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 Qy 473 TTACGCTCTAAATAAAAAAAAAAAAAAAAAAAAAA 506
 Db 502 TTACGCTCTATATGTAATAAAAAAAAAAAAAAAAAAAAAA 535

RESULT 15
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 LOCUS KS01069H01 KS01 Capsicum annuum cDNA, mRNA sequence.
 DEFINITION BM064663
 ACCESSION BM064663.1 GI:22784781
 VERSION EST
 KEYWORDS

SOURCE Capsicum annuum
 ORGANISM Capsicum annuum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Solanales; Solanaceae; Capsicum.

REFERENCE 1 (bases 1 to 522)
 Lee,S., Kim,S.-Y., Chung,Y.-H., Shin,H.-J., Goh,S.-H., Pai,H.-S.,
 Hur,C.-G. and Choi,D.
 Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
 annuum L.) and Sequence Analysis in Relation to Hypersensitive
 Response Against Pathogen

TITLE Unpublished
 JOURNAL Contact: Doil Choi
 COMMENT Genome Research Center and National Center for Genome Information
 Korea Research Institute of Bioscience and Biotechnology
 P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
 Tel: 82-42-860-4340
 Fax: 82-42-860-4309
 Email: doil@mail.kribb.re.kr
 High quality sequence stop: 522.

FEATURES
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 1. 522
 Location/Qualifiers
 /organism="Capsicum annuum"
 /mol_type="mRNA"
 /cultivar="Bukang"
 /db_xref="taxon:4072"

BASE COUNT 176 a 83 c 97 g 181 t
 ORIGIN
 Query Match 70.5%; Score 356.8; DB 12; Length 537;

/cissue_type="leaf inoculated with Xanthomonas campestris
pv. glycines"
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/clone_lib="KS01"
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Best Local Similarity 88.1%; Pred. No. 2.9e-33;
Matches 446; Conservative 0; Mismatches 44; Indels 16; Gaps 5;

QY 2 AAGAGCTATGGCTGCTTCATTACTTATGCGCATTTCTTGTGGCAATGACACTCT 61
DB 25 AAGAGCTATGGCTGCTTCATTACTTATGCGCATTTCTTGTGGCAATGACACTCT 84
QY 62 TTGTTGCTATGGGTCAGAGGAGGAAATTTGCTTAAGGCTCAAAACCTGTTA 121
DB 85 TTGTTGCTATGGGTCAGAGGAGGAAATTTGCTTAAGGCTCAAAACCTGTTA 144
QY 122 AATGTCATGAGCCCTCTATGTCAAAACCTGATGAGAGGAAATATGAAAGATG 181
DB 145 TATGACTATATGACCTCAATGCAAAAGCACTCTGT--TCAAGGTGAATATGAAAGATG 201
QY 182 GTCAATTTGTCACATCTTAAGCAAGTCTTATGCAAGAGATGT-----AATGCTA 235
DB 202 GTCAATTTGTCACATCTTAAGCAAGTCTTATGCAAGATGTGTTCAGAGATGCTA 261
QY 236 AAACCTGCGACAGCAATTTGCTGTCGAGAGAGTTCCCAAGCAGTAATTAAGTTTG 295
DB 262 AAACCTGCGACAGCAAA---TTGCTTGAAGAGAGTTTCTCAAGCAGTAAATTTA 317
QY 296 ATTATGATTTAGTGTCAACAAAATTAATTAAGTGTGCTTTCTTAAAGGTAAC 355
DB 318 ATTATGATTTAGTGTCAACAAAATTAATTAAGTGTGCTTTCTTAAAGGTAAC 377
QY 356 TATATGTTGTATTTGCTGTATAGTCCATTGACACATTAATTAAGTTGTGACA 415
DB 378 TATTAAGTTGTATTTGCTGTATAGTCCATTGACACATTAATTAAGTTGTGACA 436
QY 416 CATCAATCCTTATGATCTTATTAAGTTGTGTG--TTTAAATGAAGAGATCGTT 473
DB 437 CATCAATCCTTATGATCTTATTAAGTTGTGTGTTTAAATGAAGAGATCGTT 496
QY 474 TACGCTTAATAAAAAAAAAAAAAA 499
DB 497 TACGCTCAAAAAAAAAAAAAA 522

Search completed: August 23, 2003, 07:03:28
Job time : 1931 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 23, 2003, 05:52:23 ; Search time 160 Seconds

(without alignments)
7109.818 Million cell updates/sec

Title:

US-09-854-562-1

Perfect score:

1 aaagagactatgctcgttc.....aaaaaAAAAAAAAAAAAA 506

Sequence:

IDENTITY NUC

Scoring table:

Gapop 10.0 , Gapext 1.0

Searched:

1517243 seqs, 1124081882 residues

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
1	93.8	18.5	564	9	US-09-777-347-1	Sequence 1, Appl1
2	62.6	12.4	3528	9	US-09-777-347-2	Sequence 2, Appl1
3	50.4	10.0	1210	14	US-10-078-090-28	Sequence 248, Appl1
4	49.8	9.8	7669	12	US-10-311-455-602	Sequence 602, Appl1
5	48.4	9.6	393	14	US-10-066-543-593	Sequence 593, Appl1
6	48	9.5	2682	9	US-09-925-299-70	Sequence 70, Appl1
7	48	9.5	2682	11	US-09-925-299-70	Sequence 70, Appl1
8	47.2	9.3	5675	12	US-10-106-698-248	Sequence 148, Appl1
9	47.2	9.3	5675	12	US-10-311-455-1249	Sequence 1249, Appl1
10	47	9.3	240	10	US-09-878-574-7281	Sequence 7281, Appl1
11	47	9.3	250	10	US-09-878-574-7285	Sequence 7285, Appl1
12	46	9.1	424	14	US-10-198-846-2925	Sequence 2925, Appl1
13	45.8	9.1	1667	14	US-10-220-380-7	Sequence 7, Appl1
14	45.4	9.0	9510	12	US-10-240-485-115	Sequence 115, Appl1
15	45.2	8.9	6074	14	US-10-172-086-44	Sequence 44, Appl1
16	43.6	8.6	17721	12	US-10-311-455-1702	Sequence 1702, Appl1

17	43.4	8.6	318	10	US-09-960-352-6482	Sequence 6482, Appl1
18	43.4	8.6	944	14	US-10-103-313-151	Sequence 151, Appl1
19	43.4	8.6	1975	14	US-10-198-846-11553	Sequence 11553, Appl1
20	43.2	8.5	666	9	US-09-770-149-280	Sequence 280, Appl1
21	43.2	8.5	2000	10	US-09-938-8428-4017	Sequence 4017, Appl1
22	43.2	8.5	6219	12	US-10-311-455-839	Sequence 839, Appl1
23	43	8.5	2505	9	US-09-729-674-198	Sequence 198, Appl1
24	43	8.5	10329	12	US-10-311-455-2096	Sequence 2096, Appl1
25	43	8.5	16724	12	US-10-311-455-1064	Sequence 1064, Appl1
26	43	8.5	16724	12	US-10-240-485-90	Sequence 90, Appl1
27	43	8.5	17421	12	US-10-240-453-56	Sequence 56, Appl1
28	43	8.5	17421	14	US-10-239-676-54	Sequence 115, Appl1
29	42.8	8.5	1797	11	US-09-974-879-115	Sequence 115, Appl1
30	42.8	8.5	1797	11	US-09-305-736-116	Sequence 116, Appl1
31	42.8	8.5	2254	13	US-10-114-893-211	Sequence 211, Appl1
32	42.6	8.4	638	9	US-09-764-869-351	Sequence 351, Appl1
33	42.6	8.4	638	14	US-10-091-504-351	Sequence 351, Appl1
34	42.6	8.4	726	11	US-09-764-891-8400	Sequence 8400, Appl1
35	42.4	8.4	2270	10	US-10-042-894A-24	Sequence 24, Appl1
36	42.4	8.4	2814	10	US-09-880-107-3419	Sequence 3419, Appl1
37	42.4	8.4	2814	10	US-09-967-768A-191	Sequence 191, Appl1
38	42.4	8.4	2814	14	US-10-223-085-335	Sequence 335, Appl1
39	42.4	8.4	2814	14	US-10-223-084-335	Sequence 335, Appl1
40	42.4	8.4	2814	14	US-10-223-088-335	Sequence 335, Appl1
41	42.4	8.4	2814	14	US-10-223-090-335	Sequence 335, Appl1
42	42.4	8.4	2814	14	US-10-223-087-335	Sequence 335, Appl1
43	42.4	8.4	2814	14	US-10-223-083-335	Sequence 335, Appl1
44	42.4	8.4	2814	14	US-10-223-089-335	Sequence 335, Appl1
45	42.4	8.4	4657	9	US-09-764-870-239	Sequence 239, Appl1

ALIGNMENTS

RESULT 1
US-09-777-347-1
Sequence 1, Application US/09777347
Patent No. US20010014977A1

GENERAL INFORMATION:
APPLICANT: McBratide, Kevin E.
Stalker, David M.
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: Calgene, Inc.
STREET: 1920 Fitch Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/777,347
FILING DATE: 05-Feb-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,087
FILING DATE: 17-JUL-90
APPLICATION NUMBER: USSN 07/554,195
FILING DATE: 19-JUL-89
APPLICATION NUMBER: USSN 07/382,518

ATTORNEY/AGENT INFORMATION:
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 91-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510

INFORMATION FOR SEQ ID NO: 1
 SEQUENCE CHARACTERISTICS:
 LENGTH: 564 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 1
 US-09-777-347-1

Query Match 18.5%; Score 93.8; DB 9; Length 564;
 Best Local Similarity 61.2%; Pred. No. 1e-12; Indels 77; Gaps 8;
 Matches 330; Conservative 0; Mismatches 132;

8 CTATGCTCTGCTTCATTTACTTCATGCGATTTCTGTCTGGCAATGACACTCTTTGTTG 67
 38 CCATGGCTGCTTCATTTCTTCATGCGATTTTGTCTGGCAATGATGCTCTTTGTTA 97
 68 CTTATGGGTCAGAGGCAAGAAATTTGC---TGTAAAGCTCACAACCTGTTAAAT 124
 98 CCTATGAGGTAGAACCTCAGCAAAATTTGCAAGCACCAAGCCAACTTCCAGGATTAT 157
 125 GTTCTAGTACCCCTATGTCAAAAACCTGTATGAGAGAGAAATATGAGATGGTC 184
 158 GTTTATGACATCATCATGTAGAAAATTTGAT---CAAGAGAAATTTACTGGTGAC 214
 185 ATTGTTCAACATCTTAAGCAAGCTTATGATGATGAGATGTAATCTAAACTCTCG 244
 215 ATTGAGCAAACTCAAGAAAGTGTATGACATGACATGATGATTTTGAACAAATCT 274
 245 CAACAGAT---GCTTGGCTTG 263
 275 CAAGTGAAGTAAAGCAACTTGGGTGAGAAACAAAACCTTAAGTGAAGTGTGCTTG 334
 284 AAGAAGTCTCTCAAGCATAT---TAAGTTGATTAAGTATTAAGT--- 311
 335 AAGAAGATATATGATGAGATTAATTAAGTGAAGTAAATTAAGATTTTGAGTGTCA 394
 312 --CACACAAATTAATTAAGTGTGCTTTCTTAAGAGGTAACCTTAATTAAGTGTG---T 366
 395 AAAAAACAAATTAATTAAGTGTGCTTTCTTAAGGTAAGTGTGATGATGTTGTT 454
 367 ATTCTGTGATAGTATGACCATTTGACACATTAATTAAGTGTGACACATCACTCTT 426
 455 AGTATTTGCTTAAGTATGACCATTTGACACATTAATTAAGTGTGACACATCACTCTT 513
 427 CATGATCTCTATTAAGTGTGTTTAAAGAGATGCTTTAAGGCTTAATA 485
 514 C-----TTATGTATGTATGTTTAAAGAAATGATCACTACATCTTTAA 560

RESULT 2
 US-09-777-347-2
 Sequence 2, Application US/09777347
 Patent No. US20010014977A1

GENERAL INFORMATION:
 APPLICANT: Mcbride, Kevin E.
 TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Calgene, Inc.
 STREET: 1920 Fifth Street
 CITY: Davis
 STATE: CA
 COUNTRY: USA
 ZIP: 95616
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
 OPERATING SYSTEM: Macintosh 7.1
 SOFTWARE: Microsoft Word 5.1 (a)
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/777.347
 FILING DATE: 05-Feb-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/487,087
 FILING DATE: <Unknown>
 APPLICATION NUMBER: USSN 07/554,195
 FILING DATE: 17-JUL-90
 APPLICATION NUMBER: USSN 07/382,518
 FILING DATE: 19-JUL-89

ATTORNEY/AGENT INFORMATION:
 NAME: Carl J. Schneider
 REGISTRATION NUMBER: 36,924
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (916) 753-6313
 TELEFAX: (916) 753-1510

INFORMATION FOR SEQ ID NO: 2
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3528 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: genomic DNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 2
 US-09-777-347-2

Query Match 12.4%; Score 62.6; DB 9; Length 3528;
 Best Local Similarity 64.8%; Pred. No. 6e-05;
 Matches 147; Conservative 0; Mismatches 64; Indels 16; Gaps 3;

262 TGAAGAGCTTCTCAAGCATTAATTAAGTTGATTAAGATTTAGTGCACACAAAT 321
 3165 TGAAGAGTAAATTAATTAAGTGAAGTTAAATTAAGATTTAGTGCACACAAAT 3224
 322 TAAATTAAGTGTGCTTCTTAAGGCTAATTAAGTGTATTC---TTGGTGA 378
 3225 TAAATTAAGTGTGCTTCTTAAGGCTAATTAAGTGTATTC---TTGGTGA 384
 379 TAGAGCATTTGACACATTAATTAAGTGTGACATCAATCTCATGATCTTCT 438
 3285 TAGAGCATTTGACACATTAATTAAGTGTGACATCAATCTCATGATCTTCT 3332
 439 ATTAAGTGTGCTTCTTAAGGAGATGCTTTAAGGCTTAATA 485
 3333 -TTATGATGATGATTTTAAAGAAATGATGACATGATGATCTTTAA 3378

RESULT 3
 US-10-078-090-28

Sequence 28, Application US/10078090
 Publication No. US20030044815A1
 GENERAL INFORMATION:
 APPLICANT: Salcedo, Susana
 APPLICANT: Macina, Roberto
 APPLICANT: Hu, Ping
 APPLICANT: Recipon, Herve
 APPLICANT: Kaira, Kalpana
 APPLICANT: Cafierkey, Robert
 APPLICANT: Sun, Yongming
 APPLICANT: Liu, Chenghua
 TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
 FILE REFERENCE: DEX-0312
 CURRENT APPLICATION NUMBER: US/10/078,090
 CURRENT FILING DATE: 2002-02-14
 PRIOR APPLICATION NUMBER: 60/268,999
 PRIOR FILING DATE: 2001-02-15
 NUMBER OF SEQ ID NOS: 210
 SOFTWARE: Patent version 3.1
 SEQ ID NO 28
 LENGTH: 1210
 TYPE: DNA
 ORGANISM: Homo sapien

FEATURE:
NAME/KEY: misc feature
LOCATION: (631)..(631)
OTHER INFORMATION: a, c, g or t
US-10-078-090-28

Query Match 10.0%; Score 50.4; DB 14; Length 1210;
Best Local Similarity 52.9%; Pred. No. 0.03;
Matches 108; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 303 ATTAGTGTACACAAATTAATTAAGTGTGCTTTCTTAAGGGAATTAATATG 362
DB 401 ATGCATCACACGTAATTTATGTAATGTAATTAATTAATTAATTAATTAAT 460
QY 363 TTGTAATCTTGTGTATAGTACCAATTTGACACATTAATTAAGTTGTGACATCAT 422
DB 461 TTGAAATGATGCAAAATTTATGCGCATGCTGATGGAAGTCTACTGTAATATAA 520
QY 423 CCTCATGTATCTTCTATTAGTTGTGTGTTTAATGAAGAAGATGTTACGCTCA 482
DB 521 AGTCACGTATTTGCAATTAATTTCTTTCTTAATTAATTAATTAATTAATTAAT 580
QY 483 AAAAAAAAAAAAAAAAAAAAAA 506
DB 581 AAAAAAAAAAAAAAAAAAAAAA 604

RESULT 4
US-10-311-455-602/c
Sequence 602, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detect
FILE REFERENCE: 5013.1014
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: US/10/311.455
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 602
LENGTH: 7669
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-602

Query Match 9.8%; Score 49.8; DB 12; Length 7669;
Best Local Similarity 58.4%; Pred. No. 0.094;
Matches 87; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 357 ATAATGTTGATTTCTGTGATATAGTACCAATTTGACACATTAATTAAGTTGACAC 416
DB 435 ATAATATTTTATTAATTAATTAATTAATTAATTTCTTAACCTAATTAATTTTTCAT 376
QY 417 ATCAATCTTCATGATCTTCTATTAAAGTTGTGTGTTTAATGAAGAAGATCGTTAC 476
DB 375 TTAATATTTCTTAATTAATCTTAATAAATATTTTCTTTAAAAAATCTATCTTAT 316
QY 477 GGTCTAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 505
DB 315 AATAAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 287

RESULT 5

US-10-066-543-593/c
Sequence 593, Application US/10066543
Publication No. US20030087818A1
GENERAL INFORMATION:
APPLICANT: Liang, Yugu
APPLICANT: Pyle, Ruth A.
APPLICANT: Xu, Jiangchun
APPLICANT: Indrias, Carol Yoseph
APPLICANT: Lodes, Michael J.
APPLICANT: Secrest, Heather
APPLICANT: Carter, Darick
APPLICANT: Fanger, Gary R.
APPLICANT: Smith, Carole L.
APPLICANT: Durham, Margareta
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.563
CURRENT APPLICATION NUMBER: US/10/066.543
CURRENT FILING DATE: 2002-01-31
NUMBER OF SEQ ID NOS: 3417
SOFTWARE: FastSeq For Windows Version 4.0
SEQ ID NO 593
LENGTH: 393
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: misc feature
LOCATION: 51, 53, 73, 91, 121, 128, 167, 177, 216, 225, 245, 265, 281,
LOCATION: 295, 306, 313, 333, 363, 392
OTHER INFORMATION: n = A,T,C or G
US-10-066-543-593

Query Match 9.6%; Score 48.4; DB 14; Length 393;
Best Local Similarity 47.6%; Pred. No. 0.056;
Matches 121; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 253 TTGCTGTTGAAGAAGTTCCTCAAGCACTAATTAAGTTGATTAAGATTAGTCTC 312
DB 274 TTTTTCANNAATTAATTAATTTTAAAGCANAACCAAGGAAGATTTTAATTAAT 215
QY 313 ACACAAATTAATTAATTAAGTGTGCTTTCTTAAGGGAATTAATTAATTAATTTCTT 372
DB 214 GAGCAGAAATTAATTAATTAATTTGATTAATTAATTAATTAATTAATTAATTAAT 155
QY 373 GGTGATAGTACCAATTTGACACATTAATTAATTAAGTTGTGACATCAATCTTCATCTA 432
DB 154 GCTTTTAATTTTATCAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 95
QY 433 TCTTCTAATTAAGTTGTGTGTTTAATGAAGAAGATCGTTACGGCTAATAAAAAA 492
DB 94 TCANNAATGTTAATTTCTGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 35
QY 493 AAAAAAAAAAAAAA 506
DB 34 AAAAAAAAAAAAAA 21

RESULT 6
US-09-925-299-70
Sequence 70, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925.299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556

SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 2682
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (647)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-70

Query Match 9.5%; Score 48; DB 9; Length 2682;
Best Local Similarity 49.2%; Pred. No. 0.16;
Matches 123; Conservative 1; Mismatches 126; Indels 0; Gaps 0;

QY 253 TTGCTTGGTGAAGAAGAGTTCCTCAAGCAGTAATTAAGTTGATTGATTAAGTTAGTGTGC 312
DB 2433 TTTTTCAGAAATTAATGTTTTCCTTAAAGACAAACAAAGGAAGATATTAAATTAAT 2492
QY 313 ACACAAATTAATTAAGTGTGCTTCTTAAGAGGTAATTAAATGTTGATTTCTT 372
DB 2493 GAGCAGAAATTAATCTGTGTGATTTTGTACATATCTAAATTTTATATGATGTATAT 2552
QY 373 GGTGATATGATCCATTGACACATTAATTAAGTTGACATCATCTCTTATGTA 432
DB 2553 GCTTTTAAATTTTTCATCAAAATTAAGTCACTTACCTACTTGTATACCACTGTT 2612
QY 433 TCTTCTATTAAGTTGTGTGTTTAAATGAAAAAGATCGTTACGGTCTAAAAAAAAA 492
DB 2613 TCATACATGTATTTTCTGTGTATTAATTAATTAATTAATTAATTAATTAATTAAT 2672
QY 493 AAAAAAAAAA 502
DB 2673 AAAAAAAAAA 2682

RESULT 7

US-09-925-299-70
; Sequence 70, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 2682
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (647)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-70

Query Match 9.5%; Score 48; DB 11; Length 2682;
Best Local Similarity 49.2%; Pred. No. 0.16;
Matches 123; Conservative 1; Mismatches 126; Indels 0; Gaps 0;

QY 253 TTGCTTGGTGAAGAAGAGTTCCTCAAGCAGTAATTAAGTTGATTGATTAAGTTAGTGTGC 312
DB 2433 TTTTTCAGAAATTAATGTTTTCCTTAAAGACAAACAAAGGAAGATATTAAATTAAT 2492
QY 313 ACACAAATTAATTAAGTGTGCTTCTTAAGAGGTAATTAAATGTTGATTTCTT 372
DB 2493 GAGCAGAAATTAATCTGTGTGATTTTGTACATATCTAAATTTTATATGATGTATAT 2552

QY 373 GGTGATATGATCCATTGACACATTAATTAAGTTGACACATCATCTCTTATGTA 432
DB 2553 GCTTTTAAATTTTTCATCAAAATTAAGTCACTTACCTACTTACTTAAACAGCTGTT 2612
QY 433 TCTTCTATTAAGTTGTGTGTTTAAATGAAAAAGATCGTTAGGCTTAAAAAAAAA 492
DB 2613 TCATACATGTATTTTCTGTGTATTAATTAATTAATTAATTAATTAATTAATTAAT 2672
QY 493 AAAAAAAAAA 502
DB 2673 AAAAAAAAAA 2682

RESULT 8

US-10-106-698-248/c
; Sequence 248, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 248
; LENGTH: 2682
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2036) ..(2036)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-248

Query Match 9.5%; Score 48; DB 14; Length 2682;
Best Local Similarity 49.2%; Pred. No. 0.16;
Matches 123; Conservative 1; Mismatches 126; Indels 0; Gaps 0;

QY 253 TTGCTTGGTGAAGAAGAGTTCCTCAAGCAGTAATTAAGTTGATTGATTAAGTTAGTGTGC 312
DB 250 TTTTTCAGAAATTAATGTTTTCCTTAAAGACAAACAAAGGAAGATATTAAATTAAT 191
QY 313 ACACAAATTAATTAAGTGTGCTTCTTAAGAGGTAATTAAATGTTGATTTCTT 372
DB 190 GAGCAGAAATTAATTAAGTGTGTTTGTATTAATTAATTAATTAATTAATTAATTAAT 131
QY 373 GGTGATATGATCCATTGACACATTAATTAAGTTGACATCATCTCTTATGTA 432
DB 130 GCTTTTAAATTTTTCATCAAAATTAAGTCACTTACCTACTTGTTAACCACTGTT 71
QY 433 TCTTCTATTAAGTTGTGTGTTTAAATGAAAAAGATCGTTAGGCTTAAAAAAAAA 492
DB 70 TCATACATGTATTTTCTGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 11
QY 493 AAAAAAAAAA 502
DB 10 AAAAAAAAAA 1

RESULT 9

US-10-311-455-1249
; Sequence 1249, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLER, Alexander

```

1  APPLICANT: PIERDENROCK, Christian
2  APPLICANT: BERLIN, Kurt
3  TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining the Methylation of Cytosine
4  TITLE OF INVENTION: Cytosine methylation
5  FILE REFERENCE: 5013.P014
6  CURRENT APPLICATION NUMBER: US/10/311.455
7  PRIOR FILING DATE: 2002-12-16
8  PRIOR APPLICATION NUMBER: PCT/EP01/07537
9  PRIOR FILING DATE: 2001-07-02
10 PRIOR APPLICATION NUMBER: DE 10032529.7
11 PRIOR FILING DATE: 2000-06-30
12 PRIOR APPLICATION NUMBER: DE 10043826.1
13 PRIOR FILING DATE: 2000-09-01
14 NUMBER OF SEQ ID NOS: 2424
15 SEQ ID NO 1249
16 LENGTH: 5675
17 TYPE: DNA
18 ORGANISM: Artificial Sequence
19 FEATURE:
20 OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
21 US-10-311-455-1249

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Query Match	9.3%	Score 47.2;	DB 12;	Length 5675;
Best Local Similarity	46.8%;	Pred. No. 0.34;		
Matches 148; Conservative	0;	Mismatches 168;	Indels 0;	Gaps 0;

Qy	141	TTGTCAAAAACTCTGTATGAGAGAAAGGAAATATGAATAAGTGTATGTCTTACAAATCTC	200
Db	4096	AAGGAGAAAAATAGAGAGATGAGAGAAAAATTTAGAGATGATTTGTTTTTTAATTTT	4155
Qy	201	AAGCAGAGCTTATCATGATGAAGAGATGTAAATCTTAAATCTCGCAGACAGATTGCTTGC	260
Db	4156	AAAGATTGTGTAATTTGAATTTTAAAGGAGAGGGGAAAAGTTGAAAAGGAAATAGATAT	4215
Qy	261	TTGGAAGAGAGTTCCTCAACAGATATTAAAGTTATTATGATTTAGTGCACACAAAA	320
Db	4216	GCTGTAGAAGATTAAGAGATGAGAGATTTTAAGTTCGTAGATATGTATTTATTTAGTT	4275
Qy	321	TTAAATAAAGTGTGCTCTTTCTTAAAGAGGTAACCTAATATAGTTGTAAATCTTGGTATA	380
Db	4276	TTATATATTATTATGAGAGATTACGTGGGTATTATTATTATTAATAATTCGTTATAGA	4335
Qy	381	GTAGGCATTTGACACATTAAATTTAAAGTTGTGACATCATCTTCATGATCTTCAT	440
Db	4336	ATTAAAAATTAAATTTAAAGGAAATATATTTTTTTTTTTTAAAGATTTTTTTTGTATAT	4395
Qy	441	TAAAGTTGTGCTTTT	456
Db	4396	TTTGTATAGAGTTT	4411

```

RESULT 10
US-09-878-574-7281
; Sequence 7281, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrium, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401) B
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 7281
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 70109968BH1
US-09-878-574-7281

```

Query Match 9.3%; Score 47; DB 10; Length 240;
Best Local Similarity 59.3%; Pred. No. 0.097;
Matches 80; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy	372	TGCTGTAATAGTAGCATTTGGACACATTTAAAGTTGACACATCATTCCTTATGT	431
Db	39	TGTTGTAACGTTAGTGTGTTTTGGTTTATACCAATTTTGGGAATGTAAACATTACTTT	98
Qy	432	ATCTTCATTAAGTTGCTGTTTTAATGAAGAAGATCGTTACGGTCTAAAAAAA	491
Db	99	ATCGTTTATATGCTATGCTCCAAATGAATGTATTTTCCAAAAAAA	158
Qy	492	AAAAAAAAAAAAA	506
Db	159	AAAAAAAAAAAAA	173

RESULT 11
US-09-878-574-7255
; Sequence 7255, Application US/09878574

```

/ GENERAL INFORMATION:
/ APPLICANT: Byrum, Joseph R.
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Thompson, Michael D.
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(15401)B
/ CURRENT APPLICATION NUMBER: US/09/878,574
/ CURRENT FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: 09/333,535
/ PRIOR FILING DATE: 1999-06-14
/ NUMBER OF SEQ ID NOS: 15775
/ SEQ ID NO 7255
/ LENGTH: 250
/ TYPE: DNA
/ ORGANISM: Glycine max
/ OTHER INFORMATION: Clone ID: 701099656H1
US-09-878-574-7255

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Query Match	9.3%	Score 47;	DB 10;	Length 250;
Best Local Similarity	59.3%	Pred. No. 0.098;		
Matches	80;	Conservative	0;	Mismatches 55;
			Indels	0;
			Gaps	0

OY	372	TGCTGTAATAGTAGCCATTGGACACATTAATTAAAGTTGTGACACATCAATCCCTTCATGT	431
OY			
Db	39	TGTTGTAACCTGTGTGTGTTTTGTGTTGAACCAATTTTGGGAATGTAAACATTACTTT	98
OY	432	ATCTTCATTAAGTTTGTGTGTTTAAATGAAAAGATCGTTACGGCTTAAATAAAAAA	491
OY			
Db	99	ATGCTTTTAATATCTTATCTCCAAATGAAATTGTAGCTTTATTTTCCAAAAAAA	158
OY			
OY	492	AAAAAAAAAAAAAAAAA	506
OY			
Db	159	AAAAAAAAAAAAAAAAA	173

RESULT 12
US-10-198-846-2923/C
/ Sequence 2923, Application US/10198846
/ Publication No. US2003009974A1
/ GENERAL INFORMATION:
/ APPLICANT: Lillie, James
/ APPLICANT: Xu, Yongyao
/ APPLICANT: Wang, Youzhen
/ APPLICANT: Steinhmann, Kathleen
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
/ TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
/ TITLE OF INVENTION: THERAPY OF BREAST CANCER
/ FILE REFERENCE: MRI-049
/ CURRENT APPLICATION NUMBER: US/10/0198, 846
/ CURRENT FILING DATE: 2002-07-18

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;; PRIOR APPLICATION NUMBER: 60/306,220
;; PRIOR FILING DATE: 2001-07-18
;; NUMBER OF SEQ ID NOS: 14084
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO: 2929
;; LENGTH: 424
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 149_160, 166, 167, 169, 171, 175, 181, 182, 189, 190, 192,
;; LOCATION: 197, 199, 205, 206, 208, 236, 240, 242, 252, 255, 267, 277,
;; LOCATION: 278, 289, 293, 294, 295, 296, 298, 299, 307, 308, 309, 310,
;; LOCATION: 312, 322, 329, 345, 352, 357, 374, 380, 381, 388, 390
;; OTHER INFORMATION: n = A,T,C or G
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 392_393, 421, 423, 424
;; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-2929

Query Match          9.1%; Score 46; DB 14; Length 424;
Best Local Similarity 43.7%; Pred. No. 0.21;
Matches 94; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

Qy 292 TTGATTTAGATTAGTGTACACAAATTAAAGTGTGCTTTCTTAAAGGCT 351
    |||
Db 355 TTNAGAAANNTTTTAAAAAANANATTTTNTNNNTTTTNNAN 296

Qy 352 AACTATAATGTTGATCTTGTGTATAGTGCATTTGACATTTAATTAAGTTGT 411
    |||
Db 295 NNNNAANGAATTTTGNNTTTTNTTTTNTTTTNTTAAAAAANTTTGN 236

Qy 412 GACACATCAATCCTTCATGATCTCTATTAGTTGTGTTTAAATGAAAGAGATCG 471
    |||
Db 235 GTTAAAAAATTTTNTTTTNTTTTNTTNNNTTTTNNNTTAAANNTAAAA 176

Qy 472 TTTACGGCTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 506
    |||
Db 175 NATANANNTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 141

RESULT 13
US-10-220-380-7
;; Sequence 7, Application US/10220380
;; Publication No. US20030113846A1
;; GENERAL INFORMATION:
;; APPLICANT: INCYTE GENOMICS, INC.
;; APPLICANT: LAL, Preeti
;; APPLICANT: YAO, Monique G.
;; APPLICANT: YUE, Henry
;; APPLICANT: GANDHI, Ameena R.
;; APPLICANT: TANG, Y. Tom
;; APPLICANT: KHAN, Farrah A.
;; APPLICANT: NGUYEN, Daniel B.
;; APPLICANT: POLICKY, Jennifer L.
;; APPLICANT: DAS, Debopriya
;; APPLICANT: HILLMAN, Jennifer L.
;; APPLICANT: WALIA, Narinder K.
;; APPLICANT: HAPALIA, April
;; APPLICANT: TRIBOULEY, Catherine M.
;; TITLE OF INVENTION: LIPID METABOLISM ENZYMES
;; FILE REFERENCE: PI-0050 PCT
;; CURRENT APPLICATION NUMBER: US/10/220,380
;; PRIOR FILING DATE: 2002-02-28
;; PRIOR APPLICATION NUMBER: 60/186,480; 60/190,415; 60/198,437
;; PRIOR FILING DATE: 2000-03-02; 2000-03-17; 2000-04-19
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: PERL Program
;; SEQ ID NO: 7
;; LENGTH: 1667
;; TYPE: DNA
;; ORGANISM: Homo sapiens
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;; FEATURE:
;; NAME/KEY: misc feature
;; OTHER INFORMATION: Incyte ID No. US20030113846A1 2372651CB1
US-10-220-380-7

Query Match          9.1%; Score 45.8; DB 14; Length 1667;
Best Local Similarity 59.7%; Pred. No. 0.43;
Matches 77; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 378 ATATGACCATTTTACACATTAATTAAGTTGTGACATCAATCCTTCATGATCTTC 437
    |||
Db 1518 ATATTCACACAGAAATCTTGTATCTATAGAGACTTATCATGCTTATGCGTTT 1577

Qy 438 TATTAGTTGTGTTTAAATGAAAGATCGTTTACGCTTAAAAAATTTTAAAAA 497
    |||
Db 1578 GAATATCTTATGATTTAAATTAATTTTATATGAGAAAAAATTTTAAAAA 1637

Qy 498 AAAAAAA 506
    |||
Db 1638 AAAAAAA 1646

RESULT 14
US-10-240-485-115
;; Sequence 115, Application US/10240485
;; Publication No. US20030148327A1
;; GENERAL INFORMATION:
;; APPLICANT: OLEK, Alexander
;; APPLICANT: PIEPENBROCK, Christian
;; APPLICANT: BERLIN, Kurt
;; TITLE OF INVENTION: Diagnosis of Diseases Associated with
;; TITLE OF INVENTION: Metastasis
;; FILE REFERENCE: 5013.1007
;; CURRENT APPLICATION NUMBER: US/10/240,485
;; PRIOR FILING DATE: 2002-10-02
;; PRIOR APPLICATION NUMBER: PCT/EP01/03970
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: DE 10019058.8
;; PRIOR FILING DATE: 2000-04-06
;; PRIOR APPLICATION NUMBER: DE 10019173.8
;; PRIOR FILING DATE: 2000-04-07
;; PRIOR APPLICATION NUMBER: DE 10032529.7
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: DE 10043826.1
;; PRIOR FILING DATE: 2000-09-01
;; NUMBER OF SEQ ID NOS: 202
;; SEQ ID NO: 115
;; LENGTH: 9510
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (310, 626, 692, 746, 779, 1117, 1183, 1188, 1378, 1382, 1473)
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (1523, 1935, 2923, 2931, 2943, 3423, 3690, 3707, 3842, 3856)
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (4181, 4203, 4397, 4727, 4736, 4805, 4838, 5261, 5272, 5414)
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (6104, 6313, 6694, 6698, 6836, 6851, 7445, 7457, 7501, 7512)
;; NAME/KEY: unsure
;; LOCATION: (7779, 7834, 7872, 8484, 8486, 8689, 8801, 8816)
US-10-240-485-115

Query Match          9.0%; Score 45.4; DB 12; Length 9510;
Best Local Similarity 50.2%; Pred. No. 1.2;
Matches 112; Conservative 0; Mismatches 111; Indels 0; Gaps 0;
```


Oy	AAAGAGCATGGCTGGTCCATTTACTTCAATGGCATTTCTTGCTTGGCAATGACATC	60
Db	AAAGAGCATGGCTGGTCCATTTACTTCAATGGCATTTCTTGCTTGGCAATGACATC	60
	1	
Oy	TTTGTGCTTATGGAGTCGACGCAAGAAATTTGCTGTAAAGACTCACAAAACCTGTT	120
Db	TTTGTGCTTATGGAGTCGACGCAAGAAATTTGCTGTAAAGACTCACAAAACCTGTT	120
	61	
Oy	AAATGTTCTAGTGAACCCCTCTATGTGATAAAAACTCTGTATGAGAGAGAAATATGAAGAT	180
Db	AAATGTTCTAGTGAACCCCTCTATGTGATAAAAACTCTGTATGAGAGAGAAATATGAAGAT	180
	121	
Oy	GGTCATTTGTTTCACAATCTTAAGCAAGTCTTATGCATGAAGAGATGTAAATGCTTAAAACT	240
Db	GGTCATTTGTTTCACAATCTTAAGCAAGTCTTATGCATGAAGAGATGTAAATGCTTAAAACT	240
	181	
Oy	CTGCAACAGAAATGGCTTGCTGAAGAGAGATTCTCTCAAGCAGTAATTAAGTTGATTAT	300
Db	CTGCAACAGAAATGGCTTGCTGAAGAGAGATTCTCTCAAGCAGTAATTAAGTTGATTAT	300
	241	
Oy	GGATTATAGTGCACAAAAATTAATTAAGTGTGGCTTCTTAAAGGGTAACCTTTAA	360
Db	GGATTATAGTGCACAAAAATTAATTAAGTGTGGCTTCTTAAAGGGTAACCTTTAA	360
	301	

Oy 361 TGTGTATCTTGTGTATAGTATGACCATTTGACATTAATAAGTTGTGACATCA 420
Db 361 TGTGTATCTTGTGTATAGTATGACCATTTGACATTAATAAGTTGTGACATCA 420
Oy 421 ATCTTCATGTATCTTGTATTAAGTTGTGTGTTTAAAGAAAGATCGTTTACGCTC 480
Db 421 ATCTTCATGTATCTTGTATTAAGTTGTGTGTTTAAAGAAAGATCGTTTACGCTC 480
Oy 481 TAAAAAATT 506
Db 481 TAAAAAATT 506

RESULT 2

US-08-984-320-1
Sequence 1, Application US/08984320
Patent No. 6222097
GENERAL INFORMATION:
APPLICANT: McBride, Kevin E.
APPLICANT: Stalker, David M.
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,320
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/487,087
FILING DATE: 07-JUN-95
APPLICATION NUMBER: USSN 07/998,158
FILING DATE: 29-DEC-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/554,195
FILING DATE: 17-JUL-90
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/382,518
FILING DATE: 19-JUL-89
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: 36,924
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
FAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
US-08-984-320-1

Query Match 18.5%; Score 93.8; DB:3; Length 564;
Best Local Similarity 61.2%; Pred. No. 5.5e-14;
Matches 330; Conservative 0; Mismatches 132; Indels 77; Gaps 8;
Oy 8 CTATGCTCTGTTCACTTATCTTATGACATTTCTTGTCTTGCAATGACACTCTTTGTTG 67

Db 368 CCAATGCTCTTCTTCAATTTCTTCAATGACATTTTGTGCTTGGCAATGATCTCTTGTGA 97
Oy 68 CTATGCTCTGACGACGACAAATTTGC---TGTAAAGCTCACAAACCTGTAAAT 124
Db 98 CCAATGCTCTGACGACGACAAATTTGC---TGTAAAGCTCACAAACCTGTAAAT 157
Oy 125 GTTCTAGTACCTCTTATGTCAAAACCTGTGTATGGAAGAAATATGAAAGTGTGTC 184
Db 158 GTTCTAGTACCTCTTATGTCAAAACCTGTGTATGGAAGAAATATGAAAGTGTGTC 214
Oy 185 ATGCTTCAATCTTATGACAGTCTTATGACAGTCTTATGACAGTCTTATGACAGTCTT 244
Db 215 ATGCTTCAATCTTATGACAGTCTTATGACAGTCTTATGACAGTCTTATGACAGTCTT 274
Oy 245 CAACGAAAT---GCTTGTGCTG 263
Db 275 CAATGAAATTAAGCAACTTTGGTGAAGCAAAACCTTAAGTGAAGTGTGCTG 334
Oy 264 AAGAAAGTCTCTCAACGAAAT---TAACTTGAATGATTTAGTGT--- 311
Db 335 AAGAAAGTCTCTCAACGAAAT---TAACTTGAATGATTTAGTGT---T 366
Oy 312 --CACAAATTAATTAAGTGTGCTTCTTAAAGGTAAGTCTTAAATGTTG---T 366
Db 395 AAAAAAATTAATTAAGTGTGCTTCTTAAAGGTAAGTCTTAAATGTTG---T 454
Oy 367 ATCTTGTGTATGATGACATTTGACATTAATAAGTTGTGACATCAATCTT 426
Db 455 AGTATGCTCTTATGATGACATTTGACATTAATAAGTTGTGACATCAATCTT 513
Oy 427 CATTGATCTTCTATTAAGTTGTGTTTAAAGAAAGATGCTTAAAGCTTAA 485
Db 514 C-----TTATGATGATGATGTTTAAAGAAAGATGCTTAAAGCTTAA 560

RESULT 3

US-08-487-087A-1
Sequence 1, Application US/08487087A
Patent No. 6268546
GENERAL INFORMATION:
APPLICANT: McBride, Kevin E.
APPLICANT: Stalker, David M.
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,087A
FILING DATE: 07-JUN-95
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/998,158
FILING DATE: 29-DEC-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/554,195
FILING DATE: 17-JUL-90
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/382,518
FILING DATE: 19-JUL-89
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719

NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 91-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-08-487-087A-1

Query Match 18.5%; Score 93.8; DB 3; Length 564;
Best Local Similarity 61.2%; Pred. No. 5,5e-14;
Matches 330; Conservative 0; Mismatches 132; Indels 77; Gaps 8;

```
QY 8 CTATGGCTGCTTCATTTACTTACATGAGGATTTCTGCTTGGCAATGACACTCTTTGTTG 67
DB 38 CCAATGGCTGCTTCATTTCTTCATGAGCAATTTGCTTGGCAATGAGCTCTTTGTTA 97
QY 68 CTTATGGGTCAGGCAAGCAAAATTTGC---TGTAAAGAGCTCAAAAACCTGTTAAT 124
DB 98 CCTATGAGTGAAGAGCTCAGCAAAATTTGCAAGCAAGCAAACTTTCCAGATTAAT 157
QY 125 GTTCTAGTACCCTCTATGTCAAAACTCTGTATGAGAGAGAGAAATATGAAATGTC 184
DB 158 GTTATATGACTCATCATGTAGAAAATATTGTAT---CAAAGAGAAATTTACTGGTGAC 214
QY 185 ATTGTTTACAAATCCTAGCAAGGCTTATGATGAAGATGAATGCTAAATCTCG 244
DB 215 ATTGAGCAAACTCCAAAGAGAGTGTATGACCTAACCTGATTTTGAACAAATCT 274
QY 245 CAACAGAAAT-----GTTGCTTG 263
DB 275 CAAAGTGAAGTAAAGCAACTTTGGGTGAAGAGCAAAACTCTAAGTGAAGTGTGCTG 334
QY 312 --CACACAAATTAATAAGTGTGCTTTCTTAAAGGTAATTTAATGTTG---T 366
DB 395 AAAAAGAGATTAATGAAGTGTGCTTTCTTAAAGGTAATTTAATGTTGTT 454
QY 427 CATGATCTTCTATTAAAGTGTGTTTAAAGAAAGATCGTTTACGGTCTAA 485
DB 514 C-----TTATGTATGTATGTTTAAATGAAGAAATGATGACATGATCTTTAA 560
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RESULT 4
US-08-397-653B-1
Sequence 1, Application US/08397653B
Patent No. 6329570
GENERAL INFORMATION:
APPLICANT: Martineau, Belinda
TITLE OF INVENTION: COTTON MODIFICATION USING
TITLE OF INVENTION: OVARY-TISSUE TRANSCRIPTIONAL
FACTORS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,653B
FILING DATE: 28-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-08-397-653B-1

Query Match 18.5%; Score 93.8; DB 4; Length 564;
Best Local Similarity 61.2%; Pred. No. 5,5e-14;
Matches 330; Conservative 0; Mismatches 132; Indels 77; Gaps 8;

```
QY 8 CTATGGCTGCTTCATTTACTTACATGAGGATTTCTGCTTGGCAATGACACTCTTTGTTG 67
DB 38 CCAATGGCTGCTTCATTTCTTCATGAGCAATTTGCTTGGCAATGAGCTCTTTGTTA 97
QY 68 CTTATGGGTCAGGCAAGCAAAATTTGC---TGTAAAGAGCTCAAAAACCTGTTAAT 124
DB 98 CCTATGAGTGAAGAGCTCAGCAAAATTTGCAAGCAAGCAAACTTTCCAGATTAAT 157
QY 125 GTTCTAGTACCCTCTATGTCAAAACTCTGTATGAGAGAGAGAAATATGAAATGTC 184
DB 158 GTTATATGACTCATCATGTAGAAAATATTGTAT---CAAAGAGAAATTTACTGGTGAC 214
QY 185 ATTGTTTACAAATCCTAAGCAAGTCTTATGCAATGAAGATGTAATGCTAAATCTCG 244
DB 215 ATTGAGCAAACTCCAAAGAGAGTGTATGACCTAACCTGATTTTGAACAAATCT 274
QY 245 CAACAGAAAT-----GTTGCTTG 263
DB 275 CAAAGTGAAGTAAAGCAACTTTGGGTGAAGAGCAAAACTCTAAGTGAAGTGTGCTG 334
QY 312 --CACACAAATTAATAAGTGTGCTTTCTTAAAGGTAATTTAATGTTG---T 366
DB 395 AAAAAGAGATTAATGAAGTGTGCTTTCTTAAAGGTAATTTAATGTTGTT 454
QY 427 CATGATCTTCTATTAAAGTGTGTTTAAAGAAAGATCGTTTACGGTCTAA 485
DB 514 C-----TTATGTATGTATGTTTAAATGAAGAAATGATGACATGATCTTTAA 560
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RESULT 5
5175095-1
Patent No. 5175095

OPERATING SYSTEM: Macintosh 7.1

SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,087A
FILING DATE: 07-JUN-95
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/998,158
FILING DATE: 29-DEC-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/554,195
FILING DATE: 17-JUL-90
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/382,518
FILING DATE: 19-JUL-89
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 91-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-487-087A-2

Query Match 12.4%; Score 62.6; DB 3; Length 3528;
Best Local Similarity 64.8%; Pred. No. 2.4e-06;
Matches 147; Conservative 0; Mismatches 64; Indels 16; Gaps 3;
QY 262 TGAAGAAGAGTTCCCAAGCAGTAAATTAAGTTGATTTAGGATTTAGTCACACAAAT 321
DB 3165 TGATGGAGTAATTAATTAAGTGAAGTTAAATGAAGATTTGAGTCAAAAAACAAAT 3224
QY 322 TAAATTAAGTGTGCTTCTTTAAAGGTAATTAATTAATGTTATTC---TTGGTGA 378
DB 3225 TAAATTAAGTGTGCTTCTTTCTTATTAAGGTAAGTGTGATTTAGTATTCGCTTA 3284
QY 379 TAGTAGCATTGACACATTAAATTAAGTTGTGACACATCAATCCTTCATGATCTTCT 438
DB 3285 TAGTAGCATTGACACATTAA--TAAGTTGTGACACATCAATTC----- 3332
QY 439 ATTAAGTTGTGTTTAAATGAAGAAGATCGTTACGCTTAA 485
DB 3333 -TTATGATGATGTTTAAATGAAGAATGATCGACATCTTTAA 3378

RESULT 8
US-08-397-653B-2
Sequence 2, Application US/08397653B
Patent No. 6329570
GENERAL INFORMATION:
APPLICANT: Martineau, Belinda
TITLE OF INVENTION: COTTON MODIFICATION USING
TITLE OF INVENTION: OVARY-TISSUE TRANSCRIPTIONAL
TITLE OF INVENTION: FACTORS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
ADDRESS: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,653B
FILING DATE: 28-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4383 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-08-397-653B-2

Query Match 12.4%; Score 62.6; DB 4; Length 4383;
Best Local Similarity 64.8%; Pred. No. 2.5e-06;
Matches 147; Conservative 0; Mismatches 64; Indels 16; Gaps 3;
QY 262 TGAAGAAGAGTTCCCAAGCAGTAAATTAAGTTGATTTAGGATTTAGTCACACAAAT 321
DB 3165 TGATGGAGTAATTAATTAAGTGAAGTTAAATGAAGATTTGAGTCAAAAAACAAAT 3224
QY 322 TAAATTAAGTGTGCTTCTTTAAAGGTAATTAATTAATGTTATTC---TTGGTGA 378
DB 3225 TAAATTAAGTGTGCTTCTTTCTTATTAAGGTAAGTGTGATTTAGTATTCGCTTA 3284
QY 379 TAGTAGCATTGACACATTAAATTAAGTTGTGACACATCAATCCTTCATGATCTTCT 438
DB 3285 TAGTAGCATTGACACATTAA--TAAGTTGTGACACATCAATTC----- 3332
QY 439 ATTAAGTTGTGTTTAAATGAAGAAGATCGTTACGCTTAA 485
DB 3333 -TTATGATGATGTTTAAATGAAGAATGATCGACATCTTTAA 3378

RESULT 9
5175095-4
Patent No. 5175095
APPLICANT: Martineau, Belinda M.; Houck, Catherine M.
TITLE OF INVENTION: OVARY TISSUE TRANSCRIPTIONAL FACTORS
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/554,195
FILING DATE: 17-JUL-1990
SEQ ID NO: 4
LENGTH: 4383
5175095-4
Query Match 12.4%; Score 62.6; DB 6; Length 4383;
Best Local Similarity 64.8%; Pred. No. 2.5e-06;
Matches 147; Conservative 0; Mismatches 64; Indels 16; Gaps 3;
QY 262 TGAAGAAGAGTTCCCAAGCAGTAAATTAAGTTGATTTAGGATTTAGTCACACAAAT 321
DB 3165 TGATGGAGTAATTAATTAAGTGAAGTTAAATGAAGATTTGAGTCAAAAAACAAAT 3224
QY 322 TAAATTAAGTGTGCTTCTTTAAAGGTAATTAATTAATGTTATTC---TTGGTGA 378
DB 3225 TAAATTAAGTGTGCTTCTTTCTTATTAAGGTAAGTGTGATTTAGTATTCGCTTA 3284
QY 379 TAGTAGCATTGACACATTAAATTAAGTTGTGACACATCAATCCTTCATGATCTTCT 438

Db 3285 TAGTAGCCATTGACACATTAA-TAAGTTGTGACATCATTAATCC----- 3332
 Oy 439 ATTAAGTTGTGTGTTTATGAAAAAGAGATCGTTAGCGTTAA 485
 Db 3333 -TTAGTATGTATGTTTATATGAAAAAATGATGACTAGATCTTTAA 3378

RESULT 10

517307-1
 Patent No. 517307
 APPLICANT: HOUCK, CATHERINE M.; PEAR, JULIE R.; MARTINEAU,
 BELINDA M.; HIATT, WILLIAM
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 MODULATIONS OF ENDOGENOUS CYTOKININ LEVELS
 NUMBER OF SEQUENCES: 6
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/554,196
 FILING DATE: 17-JUL-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 382,802
 FILING DATE: 19-JUL-1989
 APPLICATION NUMBER: 188,361
 FILING DATE: 29-APR-1988
 APPLICATION NUMBER: 168,190
 FILING DATE: 15-MAR-1988
 APPLICATION NUMBER: 54,369
 FILING DATE: 26-MAY-1987
 SEQ ID NO: 1
 LENGTH: 4383
 517307-1

Query Match 12.4%; Score 62.6; DB 6; Length 4383;
 Best Local Similarity 64.8%; Pred. No. 2.5e-06;
 Matches 147; Conservative 0; Mismatches 64; Indels 16; Gaps 3;
 Oy 262 TGAAGAAGAGTCCCAAGCAGTAATTAAGTTGATTAGATTAGAGTCACACAAAT 321
 Db 3165 TGATGAGATTAATTAAGTGAAGTTGAATTAAGATTGACATCAAAAAACAAAT 3224
 Oy 322 TAAATTAAGTGTGCTTTCTTAAGGTAATTAATGTTATTC--TTGGTGA 378
 Db 3225 TATTAAGTGTGCTTTCTTAAGGTAATTAATGTTATTC--TTGGTGA 3284
 Oy 379 TAGTACCATTTGACACATTAATTAAGTTGACACATCAATCCTTCATGATCTTCT 438
 Db 3285 TAGTACCATTTGACACATTAATTAAGTTGACACATCAATCCTTCATGATCTTCT 3332
 Oy 439 ATTAAGTTGTGTGTTTATGAAAAAGAGATCGTTAGCGTTAA 485
 Db 3333 -TTAGTATGTATGTTTATATGAAAAAATGATGACTAGATCTTTAA 3378

RESULT 11

US-08-171-385-14/C
 Sequence 14, Application US/08171385
 Patent No. 5527884
 GENERAL INFORMATION:
 APPLICANT: Mary E. Russell
 APPLICANT: Urike Utans
 TITLE OF INVENTION: Mediators of Chronic Allograft
 TITLE OF INVENTION: Rejection
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM PS/2 Model 502 or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/171,385
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Fraser, Janis K.
 REGISTRATION NUMBER: 34,819
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 350
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-08-171-385-14

Query Match 9.0%; Score 45.4; DB 1; Length 350;
 Best Local Similarity 53.0%; Pred. No. 0.02;
 Matches 97; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Oy 324 AATAAGTTGCTCTCTTAAAGGTAATTAATGTTGATCTTGGTGAATGTA 383
 Db 194 ATTAAGTTGATTAATTAATTAATTAAGAAAGAAAGGTTGTTCTTAATCTGAGTGG 135
 Oy 384 GCCATTGACACATTAATTAAGTTGACACATCAATCCTTCATGTTATTA 443
 Db 134 ATTAATTTGCTCATTAATTAATTAATTCAGATTCATCAATTTCTTAAGTTGATTA 75
 Oy 444 GTTGTGTGTTTATGAAAAAGAGATCGTTAGCGTTAAAAA 503
 Db 74 TTCAATTAAGCTTAATTAATTAATTAATTAATGTTGTTGTTAAAAA 15
 Oy 504 AAA 506
 Db 14 AAA 12

RESULT 12

US-08-361-441B-14/C
 Sequence 14, Application US/08361441B
 Patent No. 6077948
 GENERAL INFORMATION:
 APPLICANT: Russell, Mary E.
 APPLICANT: Utans, Urike
 TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION
 NUMBER OF SEQUENCES: 43
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSO for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/361,441B
 FILING DATE: 21-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/171,385
 FILING DATE: 21-DEC-1993

US-08-361-441B-27

Query Match 8.7%; Score 43.8; DB 3; Length 340;
Best Local Similarity 52.5%; Pred. No. 0.049;
Matches 96; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 324 AATAAGTGTGCTTCTTAAGGCTTAATGTTGATATCTTCTTGGTATAGTA 383
DB 196 ATTAAAGCTTGAATTTATATTAAGAAAGAACATGTGTCTTATTTCTGAGTCTGG 137
QY 384 GCCATTGACACATTAATTAAGTTGACACATCAATCTTCATGTATCTTATTA 443
DB 136 ATTATTTGCTCATATAATAATTCAGATCCATCAATTTCTCATAGTTGATAT 77
QY 444 GTTGTGTGTTTAATGAAGAGATCGTTACGCTTAAGAAAAA 503
DB 76 TTCATTATGGCTAAATAAATCTGTGTATGTACTTAAGAAAAA 17
QY 504 AAA 506
DB 16 AAA 14

RESULT 15

US-09-388-743-17
; Sequence 17, Application US/09388743
; Patent No. 6423886
; GENERAL INFORMATION:
; APPLICANT: Singletary, George
; APPLICANT: Zhou, Ian
; TITLE OF INVENTION: No. 6423886 Starch Synthase Polynucleotides and Their
; FILE REFERENCE: 1144
; CURRENT APPLICATION NUMBER: US/09/388,743
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 2274
; TYPE: DNA
; ORGANISM: Typha latifolia
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (115)...(1956)
US-09-388-743-17

Query Match 8.3%; Score 42; DB 4; Length 2274;
Best Local Similarity 62.3%; Pred. No. 0.19;
Matches 66; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 401 ATTAAGTTGACACATCAATCTTCATGTATCTTATTAAGTTGTGTTTATG 460
DB 2159 AATAATCTCTGTAATCTCTATCTTAATTATGCTATGTAATAATGTGATACA 2218
QY 461 AAAAGAGATCGTTACGCTTAAGAAAAA 506
DB 2219 AATAAGCTAGTTCTTCTTAAGAAAAA 2264

Search completed: August 23, 2003, 07:04:44
Job time : 58 secs

Tomato p2130 genome
Calgene Lambda 1400
Plasmid p2130 cDNA
p2130 contig. Calgene
Calgene lambda 1400
Calgene lambda 1400
Calgene lambda 1400
Human breast specific
Human immune system
Human angiogenesis
Human angiogenesis
Breast cancer mark-
Human colon cancer
Human colon cancer
Human immune system
Human GDP-mannose
Human GDP-mannose
Human breast cancer
cDNA encoding novel
Human lipid metabo
Human cDNA clone (1
Human cDNA sequenc
Rat allograft infla
Rat allograft infla
Tumour suppressor
Human metastasis a
Human prostate exp
Human prostate exp
Human DNA for str
Human cervical can
cDNA encoding nove
Human cervical can
Human prostate exp
Tumour suppressor
Rat allograft infla
Rat allograft infla

PI Oh B, Ko MK, Shin B, Chung CH,
 XX WPI: 2001-357927/38.
 DR P-PSDB; AAB85079.
 XX
 PT New pathogen induced genes (pepper defensin protein gene and pepper
 thionin-like protein gene) from Capsicum annuum, useful for producing
 PT transgenic plants with enhanced resistance against phytopathogens, e.g.
 PT fungi or nematode
 XX
 PS Claim 3; Page 10-11; 22pp; English.
 CC The invention provides new isolated nucleic acid molecules encoding a
 CC pepper defensin protein (PepeDef) and a pepper thionin-like protein
 CC (PepeThi). The PepeDef and PepeThi genes are useful for producing transgenic
 CC plants that exhibit enhanced resistance against phytopathogens, e.g.
 CC fungi, bacteria, viruses, nematode, mycoplasma-like organisms, parasitic
 CC higher plants, flagellate protozoa or insects. The present sequence
 CC represents the cDNA sequence of the PepeDef gene.
 XX
 SQ Sequence 506 BP; 174 A; 74 C; 96 G; 162 T; 0 other;
 Query Match 100.0%; Score 506; DB 22; Length 506;
 Best Local Similarity 100.0%; Pred. No. 3.9e-98;
 Matches 506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGAGCTATGCTGCTTCATTACTTCATGAGCATTTCTTCTGGCAATGACATC 60
 DB 1 AAAGAGCTATGCTGCTTCATTACTTCATGAGCATTTCTTCTGGCAATGACATC 60
 QY 61 TTTGTTGCTTATGGGGTGCAAGGCAAGAAATTTGCTTAAAGACTCACAAAACCTGTT 120
 DB 61 TTTGTTGCTTATGGGGTGCAAGGCAAGAAATTTGCTTAAAGACTCACAAAACCTGTT 120
 QY 121 AAATGTTCTAGTGACCTCTATGTCAAAACTCTGTATGAGAGAGAGAAATATGAAGAT 180
 DB 121 AAATGTTCTAGTGACCTCTATGTCAAAACTCTGTATGAGAGAGAGAAATATGAAGAT 180
 QY 181 GGTCAATGTTTCAACATCTTAAGCAAGTCTTATGCAATGAGAGATGTAATGCTTAAACT 240
 DB 181 GGTCAATGTTTCAACATCTTAAGCAAGTCTTATGCAATGAGAGATGTAATGCTTAAACT 240
 QY 241 CTCGCAACAGATGCTGCTTGAAGAGAGTCTCTCAAGCAATTAAGTTGATAT 300
 DB 241 CTCGCAACAGATGCTGCTTGAAGAGAGTCTCTCAAGCAATTAAGTTGATAT 300
 QY 301 GGATTTAGTGCACACAAAATTAATAAGTGTGCTTTCTTAAAGGTAATCTTATA 360
 DB 301 GGATTTAGTGCACACAAAATTAATAAGTGTGCTTTCTTAAAGGTAATCTTATA 360
 QY 361 TGTGTATTTCTTGTTATAGTAGGCAATTTGACATTAATTAAGTTGTGACATCA 420
 DB 361 TGTGTATTTCTTGTTATAGTAGGCAATTTGACATTAATTAAGTTGTGACATCA 420
 QY 421 ATCTTCAATGTTCTTCTTATTAAGTTGTGCTTTTAAAGAGATCGTTTACGCTC 480
 DB 421 ATCTTCAATGTTCTTCTTATTAAGTTGTGCTTTTAAAGAGATCGTTTACGCTC 480
 QY 481 TAAAAAATTT 506
 DB 481 TAAAAAATTT 506
 RESULT 2
 ABX12800
 ID ABX12800 standard; DNA; 548 BP.
 XX
 AC ABX12800;
 XX
 DT 29-MAY-2003 (first entry)
 XX
 DE DNA encoding Capsicum annuum L. cv. Hanbyul thionine.
 XX

KM Thionine; plant disease resistance; plant; gene; ds.
 XX
 XX Capsicum annuum L. cv. Hanbyul.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 52..306
 FT /*tag= a
 FT /product= "Thionine"
 FT /transl_except= (pos:64..66,aa:Thr)
 FT /transl_except= (pos:271..273,aa:Xaa)
 FT /note= "Xaa is given as "Net" in the specification"
 XX
 XX KR2002024732-A.
 XX
 XX 01-APR-2002.
 XX
 XX 26-SEP-2000; 2000KR-0056518.
 XX
 XX 26-SEP-2000; 2000KR-0056518.
 XX
 XX (KOCN-) KOREA CHUNGANG EDUCATIONAL FOUND.
 XX
 XX Hwang BG, Kim YJ, Lee SC;
 XX
 XX WPI: 2002-747901/81.
 XX
 XX P-PSDB; ABU08325.
 XX
 XX Thionine gene of capsicum annuum L. cv. hanbyul and probing method of
 XX resistance for plant diseases -
 XX
 XX Example 1; Fig 1; 14pp; Korean.
 XX
 XX The present invention relates to the thionine gene of Capsicum
 XX annuum L. cv. Hanbyul, and a probing method of resistance for
 XX plant diseases, caused by Xanthomonas campestris subsp. vesicatoria,
 XX Collectotrichum coccodes, Collectotrichum gloeosporioides and the like.
 XX The presents sequence encodes Capsicum annuum L. cv. Hanbyul thionine.
 XX
 SQ Sequence 548 BP; 188 A; 76 C; 105 G; 179 T; 0 other;
 Query Match 97.2%; Score 491.6; DB 24; Length 548;
 Best Local Similarity 98.2%; Pred. No. 4.4e-95;
 Matches 497; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 AAAGAGCTATGCTGCTTCATTACTTCATGAGCATTTCTTCTGGCAATGACATC 60
 DB 43 AAAGAGCTATGCTGCTTCATTACTTCATGAGCATTTCTTCTGGCAATGACATC 102
 QY 61 TTTGTTGCTTATGGGGTGCAAGGCAAGAAATTTGCTTAAAGACTCACAAAACCTGTT 120
 DB 103 TTTGTTGCTTATGGGGTGCAAGGCAAGAAATTTGCTTAAAGACTCACAAAACCTGTT 162
 QY 121 AAATGTTCTAGTGACCTCTATGTCAAAACTCTGTATGAGAGAGAGAAATATGAAGAT 180
 DB 163 AAATGTTCTAGTGACCTCTATGTCAAAACTCTGTATGAGAGAGAGAAATATGAAGAT 222
 QY 181 GGTCAATGTTTCAACATCTTAAGCAAGTCTTATGCAATGAGAGATGTAATGCTTAAACT 240
 DB 223 GGTCAATGTTTCAACATCTTAAGCAAGTCTTATGCAATGAGAGATGTAATGCTTAAACT 282
 QY 241 CTCGCAACAGATGCTGCTTGAAGAGAGTCTCTCAAGCAATTAAGTTGATAT 300
 DB 283 CTCGCAACAGATGCTGCTTGAAGAGAGTCTCTCAAGCAATTAAGTTGATAT 342
 QY 301 GGATTTAGTGCACACAAAATTAATAAGTGTGCTTTCTTAAAGGTAATCTTATA 360
 DB 343 GGATTTAGTGCACACAAAATTAATAAGTGTGCTTTCTTAAAGGTAATCTTATA 402
 QY 361 TGTGTATTTCTTGTTATAGTAGGCAATTTGACATTAATTAAGTTGTGACATCA 420
 DB 403 TGTGTATTTCTTGTTATAGTAGGCAATTTGACATTAATTAAGTTGTGACATCA 462
 QY 421 ATCTTCAATGTTCTTCTTATTAAGTTGTGCTTTTAAAGAGATCGTTTACGCTC 480

68 CTTATGGGGTGC³AAGGCAAGAAATTTGC--TGTAAAGAGCTCACAAAACTGTAAAT 124

PT region - useful for
PT prodn. of exogenous
v

PT region - useful for
PT prodn. of exogenous
v

ES Disclosure: Fig 1; 18pp; English.

CC The sequence given shows the DNA sequence of cDNA clone p2130. This
 CC sequence is expressed during the early stages of anthesis in tomatoes.
 CC The message is expressed in ovary integument and ovary outer pericarp
 CC tissue. It is not readily detectable in other tissues or at other
 CC stages of fruit development. The transcription initiation region
 CC associated with this gene is therefore considered to be ovary-
 CC specific. The actual function of the p2130 polypeptide is unknown.
 CC The transcription initiation region can be used for modulation of
 CC endogenous fruit products, for production of exogenous products and
 CC for modification of the phenotype of fruit and fruit products.
 CC (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 564 BP; 188 A; 80 C; 107 G; 189 T; 0 other;

Query Match 18.5%; Score 93.8; DB 14; Length 564;

Best Local Similarity 61.2%; Pred. No. 7e-11; Indels 77; Gaps 8;

Matches 330; Conservative 0; Mismatches 132.

8 CTATGGCTGCTCCATTACTTACATGCGATTTCTTGTGCAATGACACTCTTTGTTG 67
 38 CCATGGCTGCTCCATTACTTACATGCGATTTCTTGTGCAATGACACTCTTTGTTG 97
 68 CTATGGCTGCTCCATTACTTACATGCGATTTCTTGTGCAATGACACTCTTTGTTG 124
 98 CCTATGAGGTAGAACCTCAGCAAACTTTCAGCAACCACTTCCAGGATTTAT 157
 125 GTTCTAGTACCCCTATGCTCAAAACCTGATGAGAGAGAAATGAGATGCTC 184
 158 GTTTATGACATCATCATGATGAGAAATATGAT--CAAGAGAAATTTCTGCTGAC 214
 185 ATTGTTTCAACATCTTAAGCAAGTCTTATGATGAGAGAGATGATGCTTAACTCTG 244
 215 ATTGAGCAAACTCCAAAGAAAGTGTATGATGACATGACATGATTTGCAAAATCT 274
 245 CAACGAAT--GCTTGGCTTG 263
 275 CAAGGAAGTTAAACCACTTGGGTGAGAGCAAAACCTTAAGTGAAGTGGCTTG 334
 284 AAGAGAGTCTCTCAAGAGTAAT--TAAGTTGATGATGATTTAGTGT-- 311
 335 AAGAGAGATTTATGATGAGATTAATTAAGTGAAGTAAATGAGATTTGAGTGTCA 394
 312 --CACACAAATTAATAAAGTGTCTTTCTTAAAGGTAATTAATGTTG--T 366
 395 AAAAAACAATTAATAAAGTGTCTTTCTTAAAGGTAATTAATGTTG--T 454
 367 ATTCTTGTGATAGTACCATTTGACACATTAATTAAGTGTGACACATCAATCTT 426
 455 AGTATTTGCTATAGTACCATTTGACACATTAATTAAGTGTGACACATCAATCAATC 513
 427 CATGATCTTCTATTAAGTGTGTTTAAATGAAGAGAGTGTGAGGCTCAAA 485
 514 C-----TTATGATGATGATTTTAAATGAAGATGATGATGATGATGATTTAA 560

RESULT 5

AAAT31823 standard; cDNA; 564 BP.

AAAT31823;

25-MAR-2003 (updated)

14-SEP-1996 (first entry)

Tomato p2130 cDNA clone.

Ovary; ovule; fruit; tomato; cotton; melon; vector;

transgenic plant; ss.

Lycopersicon esculentum cv. UC82B.

Key Location/Qualifiers

FT CDS 1..357

US5530185-A.

25-JUN-1996.

29-DEC-1992; 92US-0998158.

29-DEC-1992; 92US-0998158.

19-JUL-1989; 89US-0382518.

17-JUL-1990; 90US-0554195.

(CALJ) CALGENE INC.

Matineau BM, Reilley AA, Stalker DM;

WPI; 1996-308822/31.

P-PSDB; AAR97559.

Example 3; Fig 1A-B; 25pp; English.

The tomato p2130 clone contains a 564 bp insert of cDNA (AAAT31823)
 detected only in a tomato cDNA library prepd. from pre-anthesis
 RNA. It was isolated by screening a library prepd. from cDNA
 of pre-anthesis stage ovaries with probes made from pre-anthesis
 mRNA, leaf mRNA and young seedling mRNA. The insert was used to
 isolate the corresponding genomic clone (AAAT31824). The p2130
 CC transcriptional initiation region is considered to be ovary-specific.
 CC It can be utilised in DNA constructs for the expression of
 CC heterologous genes, partic. in early fruit development, and esp. for
 CC expression of a melanin synthesis gene in transgenic cotton. The
 CC native function of the p2130 gene product (AAR97559) is unknown.
 CC (Updated on 25-MAR-2003 to correct PF field.)

SO Sequence 564 BP; 188 A; 80 C; 107 G; 189 T; 0 other;

Query Match 18.5%; Score 93.8; DB 17; Length 564;

Best Local Similarity 61.2%; Pred. No. 7e-11; Indels 77; Gaps 8;

Matches 330; Conservative 0; Mismatches 132.

8 CTATGGCTGCTCCATTACTTACATGCGATTTCTTGTGCAATGACACTCTTTGTTG 67
 38 CCATGGCTGCTCCATTACTTACATGCGATTTCTTGTGCAATGACACTCTTTGTTG 97
 68 CTATGGCTGCTCCATTACTTACATGCGATTTCTTGTGCAATGACACTCTTTGTTG 124
 98 CCTATGAGGTAGAACCTCAGCAAACTTTCAGCAACCACTTCCAGGATTTAT 157
 125 GTTCTAGTACCCCTATGCTCAAAACCTGATGAGAGAGAAATGAGATGCTC 184
 158 GTTTATGACATCATCATGATGAGAAATATGAT--CAAGAGAAATTTCTGCTGAC 214
 185 ATTGTTTCAACATCTTAAGCAAGTCTTATGATGAGAGAGATGATGCTTAACTCTG 244
 215 ATTGAGCAAACTCCAAAGAAAGTGTATGATGACATGACATGATTTGCAAAATCT 274
 245 CAACGAAT--GCTTGGCTTG 263
 275 CAAGGAAGTTAAACCACTTGGGTGAGAGCAAAACCTTAAGTGAAGTGGCTTG 334
 284 AAGAGAGTCTCTCAAGAGTAAT--TAAGTTGATGATGATTTAGTGT-- 311
 335 AAGAGAGATTTATGATGAGATTAATTAAGTGAAGTAAATGAGATTTGAGTGTCA 394
 312 --CACACAAATTAATAAAGTGTCTTTCTTAAAGGTAATTAATGTTG--T 366
 395 AAAAAACAATTAATAAAGTGTCTTTCTTAAAGGTAATTAATGTTG--T 454

QY 367 ATCTGGTGTATAGTGGCATTTGACACATTAAATTAAGTGGACACATCATCTT 426
 DB 455 AGTATGGCTTATAGTGGCATTTGACACATTAA-1TAGTTTGACACATCATTAATC 513
 QY 427 CATGTATCTTCTATTAAAGTTGTGTTTATGAGAAAGATGCTTACGCTTAA 485
 DB 514 C-----TTATGTATGATGTTTATGAGAAATGATGACATCATCTTTTA 560
 RESULT 6
 AAT48813 standard; cDNA; 564 BP.
 AC AAT48813;
 XX 14-MAR-1997 (first entry)
 XX CDNA clone pZ130 capable of directing ovary-tissue transcription.
 DE Ovary; fruit; colour; pigmentation; cotton; tomato; probe;
 XX promoter; pZ130; pZ7 transgenic plant; ds.
 OS Lycopersicon esculentum cv. UC82B.
 XX Key Location/Qualifiers
 FT CDS 1..357
 FT misc_RNA 447..564
 FT /tag= a
 FT /tag= b
 FT /note= "bases 447-564 correspond to clone pZ7"
 XX W09640951-A2.
 XX 19-DEC-1996.
 PD 07-JUN-1996; 96WO-US09911.
 PE 07-JUN-1995; 95US-0487087.
 XX (CALJ) CALGENE INC.
 PA MCBride K, Stalker DM;
 XX WPI: 1997-052341/05.
 DR P-PSDB; AAM08364.
 XX DNA construct capable of directing ovary-tissue transcription in
 PT plants - useful for modifying colour phenotype, in e.g. cotton
 XX Example 1; Fig 1; 75pp; English.
 PS A cDNA clone (AAT48813), designated pZ130, comprises a tomato
 CC transcriptional initiation region that is capable of directing
 CC transcription of a gene of interest specifically in plant ovary
 CC tissue, partic. early in fruit development, e.g. to modify colour
 CC phenotype. It can also be used as a molecular probe. To obtain
 CC pZ130, a tomato pre-anthesis stage cDNA library was screened by
 CC differential hybridisation. Clones pZ7 and pZ8 that hybridised
 CC only to pre-anthesis probes were used to screen a second cDNA
 CC library, yielding pZ130 and pZ70 (see also AAT48814). A genomic
 CC clone (AAT48816) was also isolated using pZ130 as probe.
 XX Sequence 564 BP; 188 A; 80 C; 107 G; 189 T; 0 other;
 XX
 Query Match 18.5%; Score 93.8; DB 18; Length 564;
 Best Local Similarity 61.2%; Pred. No. 7e-11;
 Matches 330; Conservative 0; Mismatches 132; Indels 77; Gaps 8;
 QY 8 CTATGGCTGTTCATTACTTATGAGCATTTCTGTCTTGCAATGACATCTTTGTTG 67
 DB 38 CCATGGCTGTTCATTCTTCAATGAGCATTTTGTGCTTGCAATGATGCTCTTGTGA 97

QY 68 CTATGGGCTGACAGGCAAGAAATTTGC---TTGTAAGAGCTCCACAAAACCTGTTAAAT 124
 DB 98 CTRTATGAGTGAAGAGCTCAGACAAATTTGCAAGAGCAACCAAACTTCCAGGATTAAT 157
 QY 125 GTTCTAGTGAACCTTATGTCAAAACCTGTATGAGAAAGAAATATGAAAGTGTTC 184
 DB 158 GTTTTATGACTCATCATATGAGAAATATGTAAT---CAAGAGAAATTTAATGCTGAGAC 214
 QY 185 ATGTGTTCAAAATCTTAAAGCAAGTGTCTATGATGAGAAAGATGTAATGCTAAACTGCG 244
 DB 215 ATGTGACCAAACTCCAAAGAGAGTGTCTATGCACTAAGCCATGTGATTTGACAAAATCT 274
 QY 245 CAACAGAAAT-----GTTGCTTG 263
 DB 275 CAGTGAAGTTAAAGCAACTTTGGTGAAGCAAGCAAAACTCTAAGTGAAGTGTGCTTG 334
 QY 264 AAGAGAGTTCCTCAGACAGTAAT-----TAAGTTGATTAATGATTTAGTGT----- 311
 DB 335 AAGAGAGATTAATGATGAGATTAATTAAGTGAAGTTAATAAGATTTTGAAGTCAAA 394
 QY 312 --CACACAAATTAATTAAGTGTGCTTTCTTAAAGGTTAATTAATGTTG---T 366
 DB 395 AAAAAACAAATTAATTAAGTGTGCTTTCTTAAAGGTTAATTAATGTTGTTGTT 454
 QY 367 ATCTGGTGTATAGTGGCATTTGACACATTAAATTAAGTGGACACATCATCTT 426
 DB 455 AGTATGGCTTATAGTGGCATTTGACACATTAA-1TAGTTTGACACATCATTAATC 513
 QY 427 CATGTATCTTCTATTAAAGTTGTGTTTATGAGAAAGATGCTTACGCTTAA 485
 DB 514 C-----TTATGTATGATGTTTATGAGAAATGATGACATCATCTTTTA 560

RESULT 7
 ABZ21970 standard; cDNA; 564 BP.
 ID ABZ21970;
 XX 28-MAR-2003 (first entry)
 DT Plasmid pZ130 cDNA sequence pZ7.
 XX Transcriptional factor; ovary tissue; gene; ss.
 XX Unspecified.
 OS
 XX Key Location/Qualifiers
 FT CDS 1..564
 FT /tag= a
 FT /partial
 FT /product= "pZ130 protein sequence"
 FT /trans_except= (pos:355..357,aa:Xaa)
 FT /trans_except= (pos:358..360,aa:Xaa)
 FT /trans_except= (pos:376..378,aa:Xaa)
 FT /trans_except= (pos:385..387,aa:Xaa)
 FT /trans_except= (pos:436..438,aa:Xaa)
 FT /trans_except= (pos:454..456,aa:Xaa)
 FT /trans_except= (pos:478..480,aa:Xaa)
 FT /trans_except= (pos:490..492,aa:Xaa)
 FT /trans_except= (pos:541..543,aa:Xaa)
 FT /note= "all Xaa's are encoded by stop codons"
 XX CN1189856-A.
 XX 05-AUG-1998.
 PD 07-JUN-1996; 96CN-0195170.
 XX 07-JUN-1995; 95US-0480087.
 XX (CALJ) CALGENE INC.

DR WPI: 2002-733392/80.
DR P-PSDB: AAB56255.

XX Use of transcriptional factors of ovary tissue -

XX Example 3; Fig 1A-B; 56pp; Chinese.

XX The present invention describes the use of transcriptional factors of
CC ovary tissue. The present sequence represents a nucleotide sequence
CC which is used in an example from the present invention.

XX Sequence 564 BP; 188 A; 80 C; 107 G; 189 T; 0 other;

Query Match 18.5%; Score 93.8; DB 24; Length 564;
Best Local Similarity 61.2%; Pred. No. 7e-11;
Matches 330; Conservative 0; Mismatches 132; Indels 77; Gaps 8;

```

QY 8 CTATGGCTGCTCCATTACTTCATGGCATTTCTTGTCGATGACACTCTTGTCG 67
DB 38 CCATGCTGCTGCTCCATTACTTCATGGCATTTCTTGTCGATGACACTCTTGTCG 97
QY 68 CTTATGGGCTGCAAGCAAGAAATTTGC---TGTAAAGCTCACAATACTGTTAAAT 124
DB 98 CCTATAGAGTAGAAGCTCAGCAATTTGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 157
QY 125 GTTCTATGACCTCTTATGCAAACTCTGTATGAGAAAGAAATATGAGATGCTC 184
DB 158 GTTATATGACTCATCATGTAGAAAATATTTGAT--CAAGAGAAATTTACTGCTGAC 214
QY 165 ATTGTTTACATCTTAAGCAAGCTTATGATGATGATGATGATGATGATGATGATG 244
DB 215 ATTGATGCAAACTCAGAAAGAGATGTATGATGATGATGATGATGATGATGATGATG 274
QY 245 CAACAGAAAT-----GCTTGCTG 263
DB 275 CAAGTGAAGTTTAAGCAAGCTTGGGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCT 334
QY 264 AAGAAGCTTCTCAAGCAGATAT-----TAAGTTGATATGATGATGATGATGATG 311
DB 335 AAGAAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 394
QY 312 --CAACAAATTAATAAGTGTGCTTCTTAAGAGGTAAGTAAAGTGTG---T 366
DB 395 AAAAAACAATAATAAGTGTGCTTCTTAAGAGGTAAGTAAAGTGTG---T 454
QY 367 ATTCTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 426
DB 455 AGTATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 513
QY 427 CATGATCTTCTTATTAAGTGTGCTTCTTAAGAGGTAAGTAAAGTGTG---T 485
DB 514 C-----TTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 560

```

RESULT 8
AAV70143
ID AAV70143 standard; cDNA to mRNA; 558 BP.

AC AAV70143;
DT 03-FEB-1999 (first entry)

XX Nicotiana paniculata thionine gene NpTH11.

XX Nicotiana excelsior; Nicotiana paniculata; thionine; NpTH1; NpTH2;

XX NpTH1; salt stress; resistance; ds.

XX Nicotiana paniculata.

XX Nicotiana paniculata.

XX Key Location/Qualifiers
FH 48..368
FT /+tag= a
XX

EN JP10295380-A.

XX 10-NOV-1998.

XX 23-APR-1997; 97JP-0120179.

XX 23-APR-1997; 97JP-0120179.

XX (NIBS) JAPAN TOBACCO INC.

XX WPI: 1999-038278/04.

XX P-PSDB: AAW83133.

XX Thionine gene derived by salt stress - used to deliver improved salt

XX stress to plants

XX Claim 5; Page 5-6; 6pp; Japanese.

XX The present sequence represents a thionine gene from Nicotiana
CC paniculata derived NpTH1. The thionine protein has an effect of
CC improving the salt stress resistance of a plant. The gene can improve
CC the salt stress resistance of a plant.

XX Sequence 558 BP; 175 A; 87 C; 112 G; 184 T; 0 other;

Query Match 18.2%; Score 92; DB 20; Length 558;
Best Local Similarity 57.1%; Pred. No. 1.7e-10;
Matches 275; Conservative 0; Mismatches 160; Indels 47; Gaps 4;

```

QY 1 AAGAAGCTATGCTGCTGCTTACTTCAATGATGATGATGATGATGATGATGATGATG 60
DB 39 AAGAAGCTATGCTGCTGCTGCTTACTTCAATGATGATGATGATGATGATGATGATG 98
QY 61 TTGCTGCTTATGAGGCTGCAAGCAAGAAATTTGCTGTAAGAGCTCACAATACTGTT 120
DB 99 TTGCTGCTTATGAGGCTGCAAGCAAGAAATTTGCTGTAAGAGCTCACAATACTGTT 158
QY 121 AATGTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
DB 159 GATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 218
QY 181 GGTATGTTTCAAACTTAAGCAAGGCTTATGATGATGATGATGATGATGATGATG 234
DB 219 GGAATAATGCAAAATCTCAGAAAGGCTATGATGATGATGATGATGATGATGATG 278
QY 235 AAAAAGCTGCAAGCAAGATGCT-----GCTTGCTG 256
DB 279 AAGATGATGCAAAAGAGGCTGCAAAATTTGGCCGAGAGCAAGAACTTTGGCTG 338
QY 257 TTGCTGTAAGAGGCTTCTCAAGCAGTAAATTAAGTTGATGATGATGATGATG 314
DB 339 TTGCTGTAAGAGGCTTCTCAAGCAGTAAATTAAGTTGATGATGATGATGATG 398
QY 315 ACAAATTAATAAGTGTGCTTCTTAAGAGGTAAGTAAAGTGTGATGATGATG 374
DB 399 GTCAACATTAATAAGTGTGCTTCTTAAGAGGTAAGTAAAGTGTGATGATG 458
QY 375 TGTATAGAGCATTGACATTAATAAGTGTGATGATGATGATGATGATGATG 434
DB 459 CTTTATAGAGCATTGATGATGATGATGATGATGATGATGATGATGATGATGATG 517
QY 435 TT 436
DB 518 TT 519

```

RESULT 9
AAV70142
ID AAV70142 standard; cDNA to mRNA; 566 BP.

AC AAV70142;

DT 03-FEB-1999 (first entry)

Key	Location/Qualifiers
FT	CDS
XX	1..240
XX	/*tag= a
XX	JPI0295380-A.
XX	10-NOV-1998.
XX	23-APR-1997;
XX	97JP-0120179.
XX	23-APR-1997;
XX	97JP-0120179.
XX	(N1SB) JAPAN TOBACCO INC.
XX	WPI; 1999-038278/04.
XX	P-PSDB; AAM83131.
XX	Thionine gene derived by salt stress - used to deliver improved salt stress to plants
XX	Claim 1; Page 4; 6pp; Japanese.
XX	The present sequence represents a thionine gene from Nicotiana excelsior derived Neth11. The thionine protein has an effect of improving the salt stress resistance of a plant. The gene can improve the salt stress resistance of a plant.
XX	Sequence 456 BP; 149 A; 73 C; 88 G; 146 T; 0 other;
XX	Query Match 13.3%; Score 67.2; DB 20; Length 456;
XX	Best Local Similarity 56.2%; Pred. No. 2.9e-05;
XX	Matches 244; Conservative 0; Mismatches 158; Indels 32; Gaps 5
QY	58 CTCTTTGTCCTATGGGTCGCAAGCAAGAAATTTGCTGTAAGAGCTCAAAAACCT 117
DB	1 CTCTTTGTCCTATGAGTGCAGACTGAGAAATGCGCAAGAAATTTTCA-----CT 54
QY	118 GTTAAATGTTCTAGTGACCTCTCTATGTCAAAACTCTGTATGAGAGAGAAATRTGAA 177
DB	55 GGACTATGCAATTCACATCCACAAATGCAGAAAAAGCTGTAT---CAAAGAAATTTACT 111
QY	178 GATGTCATTTGTTTCACAAATCCTTAAGCAAGTCTATGATGATGAAGATGAT---GCT 234
DB	112 GATGTCATTTGTAGCAAAATCCTCAGAGTGTCTATGCACTAACCCATGCACAGAGCT 171
QY	235 AAAACTCCGCAACGAAATGC-----TTGCTGAAGAAAGTTCCCTC 277
DB	172 GAACTTTAGCTGAGGAAGCAACAATTGGCTGCAGCTTTGCTTGAAGAAAGATATG 231
QY	278 AAGCAGTAATTAGTTGATTATGATTTAG---TGTCAACAAAAATTAATTAAGTGT 334
DB	222 GATACTAATTATGAGATTAGATAATTAATTAAGATGAGAGTGCACACATATTAAGTTCT 291
QY	335 GCCTTTCTAAAAAGGTACTTATATGTTGATCTTGTGTATATGATGACCATTTGACA 394
DB	292 ACCCTTTCTAAAAAGGTAGCTAATGTTGTGTTTAATGGCTTTAGTGCCTTTATTA 351
QY	395 CATTAAATTAAGTGTGACACATCAATCCTCAGTATCCTCTATTAGTTGTGTGT 454
DB	352 CACTTTAATTAATGATGTGGCACTTCAACCTTTGTGCAATCTTGCACTAAGTTATTGCG 411
QY	455 TTAATGAAAAAGCA 468
DB	412 TACTTTAATGAAA 425
RESULT 11	
ID	AATJ1824
AC	AATJ1824 standard; cDNA, 3528 BP.
XX	AATJ1824;
DT	25-MAR-2003 (updated)

DT 14-SEP-1996 (first entry)
 XX Tomato pZ130 genomic clone Calgene Lambda 140.
 DE Ovary; ovule; fruit; tomato; cotton; melanin; vector;
 XX transgenic plant; ss.
 KW Lycopersicon esculentum cv. UC82B.
 XX
 XX Key Location/Qualifiers
 FT misc_difference 586 /tag= a
 FT /note= "base n at position 586 is unidentified"
 FT misc_difference 590 /tag= b
 FT /note= "base n at position 590 is not identified"
 FT misc_difference 591 /tag= c
 FT /note= "base n at position 591 is not identified"
 FT misc_difference 663 /tag= d
 FT /note= "base n at position 663 is not identified"
 FT misc_difference 667 /tag= e
 FT /note= "base n at position 667 is not identified"
 FT misc_difference 769 /tag= f
 FT /note= "base n at position 769 is not identified"
 FT misc_difference 2483 /tag= g
 FT /note= "base 2483 is given as s in the specification"
 FT misc_difference 2485 /tag= h
 FT /note= "base 2485 is given as s in the specification"
 FT exon 2567..2701 /tag= i
 FT intron 2702..2921 /tag= j
 FT exon 2922..3528 /tag= k
 FT
 XX US5530185-A.
 XX
 XX 25-JUN-1996.
 XX
 XX 29-DEC-1992; 92US-0998158.
 XX
 XX 29-DEC-1992; 92US-0998158.
 XX
 XX 19-JUL-1989; 89US-0382518.
 XX
 XX 17-JUL-1990; 90US-0554195.
 XX
 XX (CALJ) CALGENE INC.
 XX
 XX Martineau BM, Reilley AA, Stalker DM;
 XX
 XX WPI; 1996-308822/31.
 XX
 XX P-PSDB; AAR97559.
 XX
 XX
 XX DNA construct for expressing melanin synthesis gene in plant ovule
 FT cells - contains promoter from the tomato pZ130 gene, also binary
 FT vector and transgenic plants, esp. cotton; contg: construct
 XX
 XX Example 5; Fig 2A-C; 25BP; English.
 XX
 XX The tomato pZ130 genomic clone (AATJ31824) was isolated from a genomic
 CC library using a pZ130 cDNA clone (AATJ31823) as probe. The pZ130
 CC transcriptional initiation region is considered to be ovary-specific.
 CC It can be utilised in DNA constructs for the expression of
 CC heterologous genes, partic. in early fruit development, and esp. for
 CC expression of a melanin synthesis gene in transgenic cotton. The
 CC native function of the pZ130 gene product (AAR97559) is unknown.

CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX Sequence 3528 BP; 1191 A; 529 C; 518 G; 1282 T; 8 other;
 SQ
 Query Match 12.4%; Score 62.6; DB 17; Length 3528;
 Best Local Similarity 64.8%; Pred. No. 0.00034;
 Matches 147; Conservative 0; Mismatches 64; Indels 16; Gaps 3;
 Oy 262 TGAAGAGAGTTCCTCAAGCAGTAATTAAGTTGATTAAGTGTGACACAAAT 321
 DB 3165 TGATGAGATTAATTAAGTGAAGTTGATTAAGTGTGACACAAAT 3224
 Oy 322 TAAATTAAGTTCCTTCTTAAGGCTAATTAATGTTATTC---TTGGTGA 378
 DB 3225 TAAATTAAGTTCCTTCTTAAAGGCTAATTAAGTGTGACACATCAATCCTGATGTTCT 3284
 Oy 379 TAGTACCATTTGACACATTAATTAAGTGTGACACATCAATCCTGATGTTCT 438
 DB 3285 TAGTACCATTTGACACATTAATTAAGTGTGACACATCAATCCTGATGTTCT 3332
 Oy 439 ATTAAGTTGTGTTTAAATGAAGAGATCGTTACGGCTTAAA 485
 DB 3333 -TTATGATGATGTTTAAATGAAGAGATCGTTACGGCTTAAA 3378
 RESULT 12
 AAT4816
 ID AAT4816 standard; cDNA; 3528 BP.
 XX
 XX AAT4816;
 XX
 XX 14-MAR-1997 (first entry)
 DT
 XX Calgene Lambda 140 genomic clone.
 DE
 XX Ovary; fruit; colour; pigmentation; cotton; tomato; probe;
 KW promoter; pZ130; pZ7; transgenic plant; ss.
 XX
 XX Lycopersicon esculentum cv. UC82B.
 XX
 XX Key Location/Qualifiers
 FT exon 2567..2701 /tag= a
 FT intron 2702..2921 /tag= b
 FT exon 2922..3528 /tag= c
 FT misc_RNA 2599..2701 /tag= d
 FT /note= "5' end of pZ130 gene"
 FT misc_RNA 2922..3382 /tag= e
 FT /note= "3' end of pZ130 gene"
 FT
 XX
 XX MO9640951-A2.
 XX
 XX 19-DEC-1996.
 XX
 XX 07-JUN-1996; 96WO-US09911.
 XX
 XX 07-JUN-1995; 95US-0487087.
 XX
 XX (CALJ) CALGENE INC.
 XX
 XX McBride K, Stalker DM;
 XX
 XX WPI; 1997-052341/05.
 XX
 XX DNA construct capable of directing ovary-tissue transcription in
 FT plants - useful for modifying colour phenotype, in e.g. cotton
 XX
 XX Example 7; Fig 2; 75bp; English.
 XX

CC Calgene Lambda 140 genomic clone (AAT4816) overlaps with the
CC tomato ovary-specific pZ130 cDNA clone (see also AAT4813) and
CC includes regions 5' and 3' to pZ130. It was isolated from a
CC tomato cv. UC82B genomic library using pZ130 as probe. The
CC genomic clone can be used to construct pZ130 promoter cassettes
CC useful for directing ovary tissue transcription in plants, e.g. to
CC modify colour phenotype in cotton.

SO Sequence 3528 BP; 1191 A; 529 C; 518 G; 1282 T; 8 other;

Query Match 12.4%; Score 62.6; DB 18; Length 3528;
Best Local Similarity 64.8%; Pred. No. 0.00034;
Matches 147; Conservative 0; Mismatches 64; Indels 16; Gaps 3;

OY 262 TGAAGAGAGTTCCTCAAGCAGTAATTAGTTGATTGTGATTTAGTGCACCAAAAT 321

DB 3165 TGATGAGTAATAATTAGTAGGTTAATAAGGATTTGATGTCACAAAAACAAAT 3224

OY 322 TAAATTAAGTGTGCTTTCTTAATAAGGTAATTATAGTTGATTC--TTGGTGA 378

DB 3225 TAAATTAAGTGTGCTTTCTTTATAGGCTTGTATGTTGTGTTAGTATGGCCTA 3284

OY 379 TAGTAGCCATTGACACATTAATTAAAGTTGTGCACATCAATCCTTCATGTAATCTTCT 438

DB 3285 TAGTAGCCATTGACACATTAAT--TAAGTTGTGCACATCAATCAATCC----- 3332

OY 439 ATTAGTTGTGTTTAAATGAAGAAGATCGTTTACGTCCTTAAA 485

DB 3333 -TTATGATGATGATGTTTAAATGAATAATGATCGATCAATCTTTAA 3378

RESULT 13

ABZ21971 ABZ21971 standard; cDNA; 3528 BP.

AC ABZ21971;

XX 28-MAR-2003 (first entry)

DE Plasmid pZ130 cDNA sequence calgene lambda 140.

XX Transcriptional factor; ovary tissue; gene; ss.

OS Unspecified.

XX CN189856-A.

PD 05-AUG-1998.

XX 07-JUN-1996; 96CN-0195170.

PR 07-JUN-1995; 95US-0480087.

PA (CALJ) CALGENE INC.

DR WPI; 2002-733392/80.

XX Use of transcriptional factors of ovary tissue -

PS Example 5; Fig 2A-C; 56pp; Chinese.

CC The present invention describes the use of transcriptional factors of
CC ovary tissue. The present sequence represents a nucleotide sequence
CC which is used in an example from the present invention.

XX Sequence 3528 BP; 1191 A; 529 C; 518 G; 1282 T; 8 other;

Query Match 12.4%; Score 62.6; DB 24; Length 3528;

Best Local Similarity 64.8%; Pred. No. 0.00034; Indels 16; Gaps 3;

Matches 147; Conservative 0; Mismatches 64; Indels 16; Gaps 3;

OY 262 TGAAGAGAGTTCCTCAAGCAGTAATTAGTTGATTGTGATTTAGTGCACCAAAAT 321

DB 3165 TGATGAGTAATAATTAGTAGGTTAATAAGGATTTGATGTCACAAAAACAAAT 3224

OY 322 TAAATTAAGTGTGCTTTCTTAATAAGGTAATTATAGTTGATTC--TTGGTGA 378

DB 3225 TAAATTAAGTGTGCTTTCTTTATAGGCTTGTATGTTGTGTTAGTATGGCCTA 3284

OY 379 TAGTAGCCATTGACACATTAATTAAAGTTGTGCACATCAATCCTTCATGTAATCTTCT 438

DB 3285 TAGTAGCCATTGACACATTAAT--TAAGTTGTGCACATCAATCAATCC----- 3332

OY 439 ATTAGTTGTGTTTAAATGAAGAAGATCGTTTACGTCCTTAAA 485

DB 3333 -TTATGATGATGATGTTTAAATGAATAATGATCGATCAATCTTTAA 3378

RESULT 14

AAQ10263 AAQ10263 standard; DNA; 4383 BP.

XX AAQ10263;

XX 25-MAR-2003 (updated)

DT 04-APR-1991 (first entry)

DE pZ130 contg. Calgene Lambda 140 genomic clone.

KM Ovary tissue transcriptional factor; DNA construct; probe;

XX clone pZ130; ss.

OS Lycopersicon esculentum UC82B.

XX Key Location/Qualifiers

FT intron 2702..2921

FT misc_RNA /*tag= a

FT /*tag= b

FT /label= pZ130

FT /note= "overlap"

FT misc_feature 2567..2567

FT /*tag= c

FT /label= transcription_start

XX EP409629-A.

PD 23-JAN-1991.

XX 19-JUL-1990; 90EP-0307926.

PR 19-JUL-1989; 89US-0382518.

PA (CALJ) CALGENE INC.

PI Martineau B, Houck CM;

DR WPI; 1991-024191/04.

XX New ovary tissue transcriptional factors - modify transcription

PT in tomato plant ovaries for use as mol. probes

XX Disclosure; Fig 2; 21pp; English.

CC To prepare pCGN2901, Calgene lambda 140 was digested with Sali

CC and the resulting fragment which contains the pZ7-hybridising

CC region was inserted into pCGN2015, at the unique Sali site.

CC pCGN2902 contains the other Sali fragment (non-pZ7-hybridising)

CC of the pZ130 genome derived from Sali digestion of

CC Calgene Lambda 140 also put into a pCGN2015 construct.

CC Plasmid DNA isolated from pCGN2901 was used in the construction

CC of a pZ130 Promoter Cassette. The promoter is ovary-specific

CC and wound-inducible in leaf cells.

CC See also AAQ10262-64.

CC (Updated on 25-MAR-2003 to correct PA field.)

SQ Sequence 4383 BP; 1539 A; 620 C; 610 G; 1606 T; 8 other;

Query Match 12.4%; Score 62.6; DB 12; Length 4383;
 Best Local Similarity 64.8%; Pred. No. 0.0035;
 Matches 147; Conservative 0; Mismatches 64; Indels 16; Gaps 3;

OY 262 TGAAGAAGAGTTCCTCAAGCAGTAATTAAGTTGATTATGATTTAGTGCACACAAAT 321
 DB 3165 TGATGAGATTAATTAATTAAGTGAAGTTAATGAAGATTTGAGTGCACAAAAACAAAT 3224
 OY 322 TAAATTAAGTGTGCTTTCTTAAGAAGTAACTATATATGTTGATTC---TTGGTGA 378
 DB 3225 TAAATTAAGTGTGCTTTCTTTATAGGTAAGTGTGATGTTGTTGTTAGTATGGCCTA 3284
 OY 379 TAGTAGCATTTGACACATTAAATTAAGTTGACACATCAATCCTTCATGATCTTCT 438
 DB 3285 TAGTAGCATTTGACACATTAA-TAAGTTGTGACACATCATTAATCC----- 3332
 OY 439 ATTAAGTTGTGTGTTTAAATGAAGAAGATCGTTACGGCTTAAA 485
 DB 3333 -TTATGTATGTATGTTTAAATGAAGAAATGATCGATCGATCTTTAA 3378

RESULT 15

ID AAQ10319 standard; cDNA; 4383 BP.

AC AAQ10319;

DT 25-MAR-2003 (updated)

DT 04-APR-1991 (first entry)

DE Calgene lambda 140 genomic clone.

KW pZ130; cytokinin; ds.

OS Synthetic.

XX Key Location/Qualifiers

FT misc_RNA 2567..3382

FT /tag= a /note= "Sequence homologous to pZ130 transcript"

FT misc_RNA 2599..3382

FT /tag= b /note= "Sequence homologous to pZ130 CDS"

FT misc_RNA 2702..2921

FT /tag= c /note= "Sequence homologous to pZ130 intron"

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

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FT

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FT

FT

FT

SQ Sequence 4383 BP; 1539 A; 620 C; 610 G; 1606 T; 8 other;

Query Match 12.4%; Score 62.6; DB 12; Length 4383;
 Best Local Similarity 64.8%; Pred. No. 0.0035;
 Matches 147; Conservative 0; Mismatches 64; Indels 16; Gaps 3;

OY 262 TGAAGAAGAGTTCCTCAAGCAGTAATTAAGTTGATTATGATTTAGTGCACACAAAT 321
 DB 3165 TGATGAGATTAATTAATTAAGTGAAGTTAATGAAGATTTGAGTGCACAAAAACAAAT 3224
 OY 322 TAAATTAAGTGTGCTTTCTTAAGAAGTAACTATATATGTTGATTC---TTGGTGA 378
 DB 3225 TAAATTAAGTGTGCTTTCTTTATAGGTAAGTGTGATGTTGTTGTTAGTATGGCCTA 3284
 OY 379 TAGTAGCATTTGACACATTAAATTAAGTTGACACATCAATCCTTCATGATCTTCT 438
 DB 3285 TAGTAGCATTTGACACATTAA-TAAGTTGTGACACATCATTAATCC----- 3332
 OY 439 ATTAAGTTGTGTGTTTAAATGAAGAAGATCGTTACGGCTTAAA 485
 DB 3333 -TTATGTATGTATGTTTAAATGAAGAAATGATCGATCGATCTTTAA 3378

Search completed: August 23, 2003, 05:57:20

Job time : 217 secs

Modulating endogenous cytokinin levels - regulatory regions are transformed into plant cells e.g. fruit to modify pheno-type

Disclosure: Fig 3; 39pp; English.

The sequence encodes an enzyme in the cytokinin biosynthetic pathway, derived from Z130, and useful in modulating a transformed plant's phenotype eg. fruit maturation, ripening etc.

(Updated on 25-MAR-2003 to correct PA field.)

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OM nucleic - nucleic search, using sw model

Run on: August 23, 2003, 02:54:57 ; Search time 1998 seconds

(without alignments)
10360.496 Million cell updates/sec

Title: US-09-854-562-1

Perfect score: 506
Sequence: 1 aaagagactatgctctgctc.....aaaaaaaaaaaaaaaaaaaaa 506

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl1.*
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
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34: em_hgt_pln.*
35: em_hgt_rtd.*
36: em_hgt_mam.*
37: em_hgt_vrt.*
38: em_hgt.*
39: em_hgt_hum.*
40: em_hgt_mus.*
41: em_hgt_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	504.4	99.7	506	8 AF112443	AF112443 Capsicum
2	494.8	97.8	548	8 AF112869	AF112869 Capsicum
3	242.8	48.0	559	8 AF128239	AF128239 Capsicum
4	106.2	21.0	601	8 AF509566	AF509566 Nicotiana
5	102.8	20.3	596	8 SLU20591	SLU20591 Solanum lyc
6	96.6	19.1	589	8 SEPT2RNA	SEPT2RNA Solanaceae
7	92	18.2	549	8 AB005250	AB005250 Nicotiana
8	92	18.2	558	8 AB005266	AB005266 Nicotiana
9	67.2	13.3	448	8 AB005265	AB005265 Nicotiana
10	56	11.1	110000	2 PFMAL7Pl_05	PFMAL7Pl_05 Capsicum
11	53.6	10.6	331039	3 AC116988	AC116988 Dictyoste
12	52.8	10.4	51729	9 AC118276	AC118276 Homo sapi
13	52.6	10.4	254050	3 PFAL984_3	PFAL984_3 Capsicum
14	52.2	10.3	110000	3 AC116984	AC116984 Capsicum
15	51.6	10.2	86826	3 BC024739	BC024739 Homo sapi
16	51.4	10.2	3764	9 AC116305	AC116305 Dictyoste
17	51.2	10.1	110000	3 AC116305_0	AC116305_0 Dictyoste
18	51.2	10.1	196490	2 AC005507	AC005507 Plasmodu
19	51	10.1	30849	3 AC117082	AC117082 Dictyoste
20	51	10.1	39575	3 AC116925	AC116925 Dictyoste
21	50.6	10.0	36148	3 AC116100	AC116100 Dictyoste
22	50.6	10.0	80804	2 AC128660	AC128660 Medicago
23	50.2	9.9	602	8 AF507976	AF507976 Petunia x
24	50	9.9	1999	8 BC020684	BC020684 Homo sapi
25	49.8	9.8	7669	6 AX345531	AX345531 Sequence
26	49.8	9.8	162539	5 AL954372	AL954372 Zebrafish
27	49.8	9.8	293431	2 PFMAL13P4	PFMAL13P4 Plasmodu
28	49.6	9.8	114226	2 AC004710	AC004710 Plasmodu
29	49.6	9.8	250421	3 AE014849	AE014849 Plasmodu
30	49.6	9.8	254733	3 AC117075	AC117075 Dictyoste
31	49.4	9.8	9751	3 AF465309	AF465309 Dictyoste
32	49.4	9.8	110000	2 PFMAL13_01	PFMAL13_01 Plasmodu
33	49.4	9.8	125958	2 AC115592	AC115592 Dictyoste
34	49.4	9.8	192581	2 PFMAL13P1	PFMAL13P1 Plasmodu
35	49.4	9.8	250663	3 AE014852	AE014852 Plasmodu
36	49.4	9.8	260929	3 AE014852	AE014852 Plasmodu
37	49.4	9.8	310779	2 AC005140	AC005140 Plasmodu
38	49	9.7	2787	3 PFSTARP	PFSTARP Plasmodu
39	49	9.7	110000	2 PFMAL7Pl_00	PFMAL7Pl_00 Capsicum
40	48.8	9.6	310	3 AS1318009	AS1318009 Allotriomi
41	48.8	9.6	1646	10 BC004087	BC004087 Mus muscu
42	48.8	9.6	3873	6 AX458573	AX458573 Sequence
43	48.8	9.6	41399	3 AC116984_5	AC116984_5 Dictyoste
44	48.8	9.6	61052	2 AC123513	AC123513 Dictyoste
45	48.8	9.6	110000	3 AC116984_4	AC116984_4 Dictyoste

ALIGNMENTS

RESULT 1	LOCUS	AF112443	506 bp	mrna	linear	PLAN 10-DEC-1999
DEFINITION	Capsicum annuum thionin-like protein (Pepthi)	mrna, complete cds.				
ACCESSION	AF112443					
VERSION	AF112443.1	GI:6552501				
KEYWORDS						
SOURCE	Capsicum annuum					
ORGANISM	Capsicum annuum					
REFERENCE	Oh,B.-Y., Ko,M.-K., Kosenyuk,I., Shin,B. and Kim,K.-S.					
AUTHORS	Oh,B.-Y., Ko,M.-K., Kosenyuk,I., Shin,B. and Kim,K.-S.					
TITLE	Coexpression of a defensin gene and a thionin-like via different					

signal transduction pathways in pepper and Colletotrichum
gloeosporioides interactions
Plant Mol. Biol. 41 (3), 313-319 (1999)
JOURNAL MEDLINE 20064969
PUBMED 10598099
REFERENCE 2 (bases 1 to 506)
AUTHORS Oh, B.J., Ko, M.K., Kostenyuk, I.A., Shin, B.C. and Kim, K.S.
TITLE Direct Submission
JOURNAL Submitted (09-DEC-1998) Kumbo Life and Environmental Science
Laboratory, Kumbo Petrochemical Co., LTD., 1 Oryong-dong, Puk-gu,
Kwangju 500-712, Korea
FEATURES
source location/Qualifiers
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10..264
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/db_xref="GI:6552502"
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BASE COUNT 173 a 75 c 96 g 162 t
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Best Local Similarity 99.8%; Pred. No. 1.8e-96;
Matches 505; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AAAGAGCTATGGCTGCTGCTTCACTTACTTCAATGCGATTCTTGTTGGCAATGACATC 60
DB 1 AAAGAGCTATGGCTGCTGCTTCACTTACTTCAATGCGATTCTTGTTGGCAATGACATC 60
QY 61 TTGTTGCTTATGGGCTGCAAGCAAGAAATTTGCTGTAAGAGCTACACAAACCTGTT 120
DB 61 TTGTTGCTTATGGGCTGCAAGCAAGAAATTTGCTGTAAGAGCTACACAAACCTGTT 120
QY 121 AAATGTTCTAGTACCCCTCTATGTCAAAACCTGTAAGAGAGAGAAATATGAAGAT 180
DB 121 AAATGTTCTAGTACCCCTCTATGTCAAAACCTGTAAGAGAGAGAAATATGAAGAT 180
QY 181 GGTCAATGTTTCAACATCTTAAGCAAGTGTATGATGATGATGATGATGATGATGAT 240
DB 181 GGTCAATGTTTCAACATCTTAAGCAAGTGTATGATGATGATGATGATGATGATGAT 240
QY 241 CTGCGAACAAGATTGCTGCTGTAAGAAAGTCTCTCAAGCAAGTAAATTAAGTTGATTAT 300
DB 241 CTGCGAACAAGATTGCTGCTGTAAGAAAGTCTCTCAAGCAAGTAAATTAAGTTGATTAT 300
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DB 301 GGATTAGTGCACAAATTAATTAAGTGTGCTTCTTAAGGGTAACCTTAAT 360
QY 361 TGTGTTATCTTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTA 420
DB 361 TGTGTTATCTTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTA 420
QY 421 ATCTCTCATGTAATCTTCTTAATTAAGTTGTGTTTAATGAAGAGATCGTTACGGTC 480
DB 421 ATCTCTCATGTAATCTTCTTAATTAAGTTGTGTTTAATGAAGAGATCGTTACGGTC 480
QY 481 TAAAAAAG 506
DB 481 TAAAAAAG 506
RESULT 2
AF112869
LOCUS AF112869 548 bp mRNA linear PLN 19-DEC-1999

DEFINITION Capsicum annuum gamma-thionin 1 precursor (thionin) mRNA, complete cds.
ACCESSION AF112869
VERSION AF112869.1 GI:6601330
KEYWORDS
SOURCE Capsicum annuum
ORGANISM Capsicum annuum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Jamids; Solanales; Solanaceae; Capsicum.
REFERENCE 1 (bases 1 to 548)
AUTHORS Hwang, B.K., Lee, S.C., Kim, Y.J. and Hong, J.K.
TITLE Molecular cloning and pathogen-induced expression of a thionin gene in pepper plants
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 548)
AUTHORS Hwang, B.K., Lee, S.C., Kim, Y.J. and Hong, J.K.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-1998) Dept. of Agricultural Biology, Korea University, Anam-dong, Sungbuk-gu, Seoul 136-701, Korea
FEATURES
source location/Qualifiers
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/db_xref="taxon:4072"
/tissue_type="leaf"
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CQKCMERKEKEDGHCFTILSKCLCMKCNKATLATELLA"
sig_peptide 52..114
/gene="thionin"
mac_peptide 115..303
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366..371
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Best Local Similarity 98.6%; Pred. No. 1.9e-94;
Matches 499; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 AAAGAGCTATGGCTGCTGCTTCACTTACTTCAATGCGATTCTTGTTGGCAATGACATC 60
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DB 61 TTGTTGCTTATGGGCTGCAAGCAAGAAATTTGCTGTAAGAGCTACACAAACCTGTT 120
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DB 181 GGTCAATGTTTCAACATCTTAAGCAAGTGTATGATGATGATGATGATGATGATGAT 240
QY 241 CTGCGAACAAGATTGCTGCTGTAAGAAAGTCTCTCAAGCAAGTAAATTAAGTTGATTAT 300
DB 241 CTGCGAACAAGATTGCTGCTGTAAGAAAGTCTCTCAAGCAAGTAAATTAAGTTGATTAT 300
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DB 301 GGATTAGTGCACAAATTAATTAAGTGTGCTTCTTAAGGGTAACCTTAAT 360

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/protein_id="AAN70999.1"
/db_xref="nci:25005087"
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mat_peptide MDN
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BASE COUNT 192 a 95 c 115 g 199 t
ORIGIN

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Best Local Similarity 57.8%; Pred. No. 1.7e-12;
Matches 322; Conservative 0; Mismatches 173; Indels 62; Gaps 5;

QY 1 AAAGAGCTATGCGCTTCCTTCACTTATGATGCAATTTCTGTTGGCAATGACATC 60
DB 52 AAAGAGCTATGCGCTTCCTTCACTTATGATGCAATTTCTGTTGGCAATGACATC 111
QY 61 TTGTTGCTTATGCGGTGCAAGCAAGCAATTTCTGTTAAAGAGCTCAAAACCTGTT 120
DB 112 TTGTTGCTTATGAGAGTGCAGATGCAATGCAAAAGCAAGCAAGCAATTTCTGGA 171
QY 121 AAATGTTCTAGTACCTCTATGCAAAAACCTGTTATGAGAGAGAGCAATATGAGAT 180
DB 172 ATATGCTATACCAACACACATGCAAGCAAGCTGTAT--CAGTGAGAAAATTTACTGAT 228
QY 181 GGTGCTATGTTACATCTCTATGCAAGCTTATGCAATGCAATGATG----- 228
DB 229 GGTGCTATGTTACATCTCTATGCAAGCTTATGCAATGCAATGATG----- 228
QY 229 AATGCTTAAACTCTGCAACAGAA 252
DB 269 AAGATGACTAAACAGAGCTGAATTTGGCTGAGCAAGCAAAACCTTGGCTGACACT 348
QY 253 TTGCTTGTCTTGA--AGAGAGCTTCTCAAGCAAGTAAATTAAGTTGATTATGATTAGT 309
DB 349 TTGCTTGAAGAGATTAATGATTAATGATTAGATTAAGCAAAATTAAGATGACAGT 408
QY 310 GTGCAACAAAATTAATAAGTGGCTTCTTAAAGGGTAACTTAAATGTTGATTT 369
DB 409 ATGACACATTAATAAGT---TTCTACCTTTCTTAAAGTGTAAAGTGTGTTTAA 464
QY 370 CTGCTGTTATGATGACCATTTGACACATTAATAAGTGTGACACATCAATCCTTAT 429
DB 455 ATTGCTTATGATGACCTTTTATACCTTAAATTAAGTGTGACATCAATCCTTATG 524
QY 430 GTATCTTCTATTAG---TTTGTGTTTAAATGAAAGAGATGCTTAAAGCTTAA 485
DB 525 CAATCTTGACATTAATTTATTTGTTACTTTAAATGAAGATGACCTTATGCTTTGG 584
QY 486 AAAAAAAAAAAAAA 502
DB 585 TTAATAAAAAAAAAA 601

RESULT 5
SLU20591 596 bp mRNA linear PLN 04-NOV-1995
LOCUS Solanum lycopersicum flower-specific gamma-chionin-like
DEFINITION U20591
VERSION U20591.1 GI:924623
ACCESSION
KEYWORDS
SOURCE
ORGANISM
Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 596)
REFERENCE
AUTHORS Milligan, S.B. and Gaesser, C.S.
TITLE Nature and regulation of p18i1-expressed genes in tomato
JOURNAL Plant Mol. Biol. 28 (4), 691-711 (1995)
MEDLINE 95375233
PUBMED 7647301
REFERENCE
2 (bases 1 to 596)
AUTHORS Milligan, S.B.

TITLE Direct Submission
JOURNAL Submitted (02-FEB-1995) Stephen B. Milligan, Molecular and Cellular
Biology, University of California at Davis, Davis, CA 95616, USA
FEATURES
SOURCE
1. 596
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/strain="VF36"
/db_xref="taxon:4081"
/clone="trp3"
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1. 56
57.374
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protein/acidic protein precursor"
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375.596
BASE COUNT 204 a 82 c 107 g 203 t
ORIGIN

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Best Local Similarity 61.5%; Pred. No. 9e-12;
Matches 343; Conservative 0; Mismatches 137; Indels 78; Gaps 8;

QY 8 CTATGCTGCTTCACTTATGATGCAATTTCTGTTGGCAATGACACTCTTTGTTG 67
DB 55 CCATGCTGCTTCACTTATGATGCAATTTCTGTTGGCAATGACACTCTTTGTTG 114
QY 68 CTATGCTGCTTCACTTATGATGCAATTTCTGTTGGCAATGACACTCTTTGTTG 124
DB 115 CCTATGAGTGAAGAGCTCAGCAATTTGCAAGAGCAAGCAAACTTTCCAGAGATTAT 174
QY 125 GTTCTAGTACCTCTATGTCAAAACCTGTATGAGAGAGCAAAATATGAGATGTC 184
DB 175 GTTTATGAGACTCATCATGTAAGAAATATTGTAT---CAAGAGAAATTTAAGTGTGAC 231
QY 185 ATTGTTTCAATCTCTAGAGAGCTTATGACAGAGAGATGTAATGCTAAATCTGCG 244
DB 232 ATTGTAGCAATCTCAAGAGAGAGTGTCTATGACTTAAGCCATGTATTTGACAAATCT 291
QY 245 CAACAGATT-----GCTTGCTTG 263
DB 292 CAATGAGTTAAAGCAACTTTGGGTGAGAGCAAAACCTAAATGAGATGTTGCTTG 351
QY 264 AAGAGAGTCTCAAGCAGTAT-----TAAGTTGATTATGATTAGTGT----- 311
DB 352 AAGAGAGATTATGATGAGTAAATTAAGTGAAGTAAATGAAGATTTTGAAGTGTCAA 411
QY 312 ---CACCAAAATTAATAAGTGTGCTTCTTAAGAGGTAACCTTAATGTTG--- 365
DB 412 AAAAAAAAAAAATTAATAAGTGTGCTTCTTAATGAGGTAACCTTATGATGTTGTTG 471
QY 366 TATCTTGTATGATGAGCAATTTGACACATTAATAAGTGTGACACATCAATCT 425
DB 472 TAGTATGCTTATGATGAGCAATTTGACACATTAATAAGTGTGACACATCAAT 530
QY 426 TCATGATCTTCTATTAAGTGTGTTTATGAGAAAGAGATGCTTAAAGCTTAA 485
DB 531 CC-----TTATGATGATGTTTAAATGAAGAAATGATGACATGATCTTAA 578
QY 486 AAAAAAAAAAAAAAAAAA 503

Db		99	TTTGTGGCTTAGAGGTGCAAGCTTAAGAAGTAACTTCGCAAAAGCAGAAACGAATCATTTCCCT	158
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Db		159	GGAATTATGCATTACCAAAACACCATGACAGAAAAAGCTTGTCAGTAGAATAATTACTGAT	218
Oy		181	GGTCAATTTGTTTCAATCCTTAAGCAAGTGTCTTATGCATGAGAGATG-----TATGCT	234
Db		219	GGAATATGTAGCAAAATCTCTCAGAAAGTGTCATTGTGTACAAACCATGTGTATTTGATGA	278
Oy		235	AAACTCTGCAACGAATTGC-----	256
Db		279	AAGATGATTCCAAAACGAGAGCTGAAAAATTTGCCGAGAAAGCAAAACTTTGGCTCACGT	338
Oy		287	TTCGTTGAAGAGAGTTCCTCAAGCAGTAAATTAAGTTGATTATGATTTAG--TGTCAC	314
Db		339	TTGCTTGAAGAGAGATGATGATGATATCTATTAATGAGATTATAGAAATTAAGATGAAGT	398
Oy		315	ACAAATTAATAATMAAGTGTGGCTTTCTTAAAAAGGTAATTATATGTGTATTTCTTGG	374
Db		399	GTCACACATTAATAAAGTGTGCTTCTTTCTTAAAAAGTACCTATGTTGTTCTTATTTGG	458
Oy		375	TGTATAGTAGCCATTGTGACACATTAATTAAGTTGTACACATCATTCCTTCACTATC	434
Db		459	CTTTAGTAGCGCTTTGTTTACCTTAAATAAG-TGTGGACATCAATCTTTGTACTT	517
Oy		435	TT 436	
Db		518	TT 519	
RESULT 8				
AB005266				
LOCUS	Nicotiana excelsior mRNA for gamma-thionin, complete cds.	558 bp	mRNA	linear
DEFINITION				PLN 05-FEB-1999
ACCESSION	AB005266			
VERSION	AB005266.1 GI:2244704			
KEYWORDS	gamma-thionin.			
SOURCE	Nicotiana excelsior			
ORGANISM	Nicotiana excelsior			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
TITLE	Asteridae; lamids; Solanales; Solanaceae; Nicotiana.			
JOURNAL	Yamada,S., Komori,T. and Inaseki,H.			
REFERENCE	CDNA cloning of gamma-thionin from Nicotiana excelsior (Accession			
AUTHORS	No. AB005266) (PCR97-131)			
TITLE	Plant Physiol. 115, 314 (1997)			
JOURNAL	2 (bases 1 to 558)			
REFERENCE	Yamada,S.			
AUTHORS	Direct Submission			
TITLE	Submitted (26-JUN-1997) Shigehiro Yamada, Plant Breeding and			
JOURNAL	Genetics Research Laboratory, Japan Tobacco Inc.; 700 Higashibara,			
REFERENCE	Iwata, Shizuko 438, Japan			
AUTHORS	(E-mail:shigehiro.yamada@pbgrl.jti.co.jp, Tel:0538-32-7116,			
TITLE	Fax:0538-32-8700)			
FEATURES				
Source	Location/Qualifiers			
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BASE COUNT	94 c 108 g 186 t			
	170 a			

ORIGIN		Query Match	18.2%	Score 92	DB 8	Length 558
Best Local Similarity		65.8%	Pred. 1.7e-09			
Matches	150	Conservative	0	Mismatches	75	Indels 3; Gaps 1
Qy	1	AAAGAGCTATGGCTGCTTCATTACTTCATGCGATTTCTTGTTGGCAATGACACTC	60			
Db	24	AAAGAACTATGGCTGCTGCTCGTGGTGGCTTCATGGCATTTGCTATCTTGGCAGTATGCTC	83			
Qy	61	TTTGTTGCTTATGGGGTGCAGGCGAAGGAATTTGCTGTGAAGCTCACAAACCTGTT	120			
Db	84	TTTGTTGCTATGATGTGGAAGCTTAAATTTGCCAAACAGAAAGCAATATCATTTCCCTGSA	143			
Qy	121	AAATGTTCTAGTGAACCTCTATGTCAAAAACCTGTGTATGAGAAAGAGAAATATGAAGT	180			
Db	144	ATATGCAATTACCAACCCACGATGAGAAAACCTGTAT---CAAAGAAAATTTTACTAT	200			
Qy	181	GGTCATTTGTCACAAATCCTTAAGCAGAGCTTATAGCATGAGAGATGT	228			
Db	201	GGTCATTTAGCAAAATCCTCAGAAAGTGTCATAGCATTAAGCCATGT	248			

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RESULT 9
AB005265 LOCUS Nicotiana excelsior mRNA for gamma-chionin, partial cds. PLN 04-JUL-1997
ACCESSION AB005265
VERSION AB005265.1 GI:2244702
KEYWORDS gamma-chionin.
SOURCE Nicotiana excelsior
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
REFERENCE
AUTHORS Yamada,S., Komori,T. and Imaseki,H.
TITLE cDNA cloning of gamma-chionin from Nicotiana excelsior
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 448)
AUTHORS Yamada,S.
TITLE Direct Submission
JOURNAL Submitted (26-JUN-1997) Shigehiro Yamada, Plant Breeding and
Genetics Research Laboratory, Japan Tobacco Inc.; 700 Higashibara,
Iwata, Shizuoka 438, Japan
(E-mail:Shigehiro.Yamada@pbgrl.jti.co.jp, Tel.:0538-32-7116,
Fax:0538-32-8700)
FEATURES
Source location/Qualifiers
1..448 /organism="Nicotiana excelsior"
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/translatio="LFAVEVQARCAREIFTGICITNPQCRKAKICEFTDGHCSKK
LRRLCTPKPGARTLAEBATTAETAELEIMDN"
BASE COUNT 141 a 73 c 88 g 146 t
ORIGIN
Query Match 13.3%; Score 67.2; DB 8; Length 448;
Best Local Similarity 56.2%; Pred. No. 0.00031;
Matches 244; Conservative 0; Mismatches 158; Indels 32; Gaps 5;

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The RPci-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.-Y., Zhao, B., Frangen, E., Taten, M., Catanes, U.J. and de Jong, P.J. (1988) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 5:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.regen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-34405, 2000 bp overlap, the clone sequenced to the right is RP11-49215, 2000 bp overlap.
Actual end of this clone is at base position 6851 of RP11-49215.

FEATURES

Source

Location/Qualifiers

1. .51729

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/mol_type="genomic DNA"

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/clone_1lb="RPci-11"

1. .143

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144. .529

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1145. .1267

/rpt_family="MIR"

1347. .1397

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ACCESSION AL929358 AL844508
VERSION      AL929358.1 GI:23505147
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
Mungall,K., Bowman,S., Atkin,R., Baker,S., Barron,A., Brooks,K.,
Buckee,C.O., Burrows,C., Cherevach,I., Chillingworth,C.,
Chillingworth,T., Christodoulou,Z., Clark,L., Clark,R., Corton,C.,
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Rabdinowitsch,E., Rajandream,M.A., Rutter,S., Rutherford,K.M.,
Sanders,M., Simmonds,M., Seeger,K., Sharp,S., Smith,R., Squares,R.,
Squares,S., Stevens,K., Taylor,K., Tivey,A., Unwin,L.,
Whitehead,S., Woodward,J., Sultson,J.E., Craig,A., Newbold,C. and
Barrell,B.G.*
Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13
Nature 419 (6906), 527-531 (2002)
12368867
JOURNAL
TITLE
JOURNALS
MEDLINE
PUBMED
AUTHORS
REFERENCES
Sander,M., Hauser,H., Baker,S., Unwin,L., Mungall,K., Berriman,M.,
Pain,A., Hall,N., Bowman,S., Churcher,C., Quail,M. and Barrell,B.
Direct Submission
Submitted (20-SEP-2002) P.falciparum Genome Sequencing Consortium,
The Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA, UK
For more information about this sequence or the Malaria Project,
see http://www.sanger.ac.uk/Projects/P_falciparum.
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    35.21% id in 213 aa, and to Escherichia coli prolyl-tRNA
    synthetase pros or dpa or b0194 SWALL:STP_ECOLI
    (SWALL:P16659) (572 aa) fasta scores: E(): 7.3e-08, 31.91%
    id in 235 aa. Pfam match to PF00587, tRNA synthetase class
    II (G, H, P, S and T)
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: August 23, 2003, 07:07:53 ; Search time 162 Seconds

(without alignments)
1151.837 Million cell updates/sec

Title: US-09-854-562-2

Perfect score: 445

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Delop 6.0 , Delext 7.0

Searched: 1517243 seqs, 1124081882 residues

Total number of hits satisfying chosen parameters: 3034486

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

Result Query Match Length DB ID Description
No. Score
1 182.5 41.0 564 9 US-09-777-347-1 Sequence 1, Appl1

SUMMARIES

RESULT 1
US-09-777-347-1
Sequence 1, Application US/09777347
Patent No. US20010014977A1
GENERAL INFORMATION:
APPLICANT: McBridge, Kevin E.
Scalder, David M.
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/777.347
FILING DATE: 05-Feb-2001
CLASSIFICATION: <Unknown>

ALIGNMENTS

2	132	29.7	3528	9	US-09-777-347-2	Sequence 2, Appl1
3	97	21.8	416	14	US-10-178-213-94	Sequence 94, Appl
4	91.5	20.6	307	14	US-10-178-213-295	Sequence 295, Appl
5	89	20.0	323	14	US-10-178-213-412	Sequence 412, Appl
6	87	19.6	363	14	US-10-178-213-124	Sequence 124, Appl
7	87	19.6	367	14	US-10-178-213-121	Sequence 121, Appl
8	86.5	19.4	272	10	US-09-878-574-10791	Sequence 10791, A
9	86.5	19.4	277	10	US-09-878-574-11794	Sequence 11794, A
10	86.5	19.4	361	10	US-09-878-574-11139	Sequence 1139, Ap
11	86.5	19.4	469	14	US-10-178-213-91	Sequence 91, Appl
12	85	19.1	466	14	US-10-178-213-385	Sequence 385, Appl
13	85	19.1	520	14	US-10-178-213-373	Sequence 373, Appl
14	83.5	18.8	275	10	US-09-878-574-14296	Sequence 14296, A
15	82	18.4	380	14	US-10-178-213-142	Sequence 142, Appl
16	81.5	18.3	447	14	US-10-178-213-136	Sequence 136, Appl
17	81	18.2	234	14	US-09-838-842A-618	Sequence 618, Appl
18	81	18.2	372	14	US-10-178-213-178	Sequence 178, Appl
19	81	18.2	373	14	US-10-178-213-202	Sequence 202, Appl
20	80	18.0	424	14	US-10-178-213-133	Sequence 133, Appl
21	80	18.0	493	14	US-10-178-213-364	Sequence 364, Appl
22	79.5	17.9	538	14	US-10-178-213-382	Sequence 382, Appl
23	79	17.8	346	14	US-10-178-213-208	Sequence 208, Appl
24	79	17.8	375	14	US-10-178-213-169	Sequence 169, Appl
25	79	17.8	378	14	US-10-178-213-190	Sequence 190, Appl
26	79	17.8	398	14	US-10-178-213-160	Sequence 160, Appl
27	79	17.8	410	14	US-10-178-213-148	Sequence 148, Appl
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29	78.5	17.6	409	14	US-10-178-213-193	Sequence 193, Appl
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35	77.5	17.4	398	14	US-10-178-213-157	Sequence 157, Appl
36	77.5	17.4	416	14	US-10-178-213-115	Sequence 115, Appl
37	77.5	17.4	416	14	US-10-178-213-118	Sequence 118, Appl
38	77.5	17.4	432	14	US-10-178-213-211	Sequence 211, Appl
39	77.5	17.4	462	14	US-10-178-213-304	Sequence 304, Appl
40	77.5	17.4	512	14	US-10-178-213-220	Sequence 220, Appl
41	77	17.3	294	9	US-09-294-093B-3064	Sequence 3064, Ap
42	77	17.3	417	14	US-10-178-213-139	Sequence 139, Appl
43	77	17.3	480	14	US-10-178-213-136	Sequence 136, Appl
44	76.5	17.2	330	14	US-10-178-213-166	Sequence 166, Appl
45	76.5	17.2	388	14	US-10-178-213-184	Sequence 184, Appl

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,087
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 07/554,195
FILING DATE: 17-JUL-90
APPLICATION NUMBER: USSN 07/382,518
FILING DATE: 19-JUL-89
ATTORNEY/AGENT INFORMATION:
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 91-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1
US-09-777-347-1

Alignment Scores:
Pred. No.: 9,15e-17 Length: 564
Score: 182.50 Matches: 41
Percent Similarity: 62.35% Conservative: 12
Best Local Similarity: 48.24% Mismatches: 29
Query Match: 41.01% Indels: 3
DB: 9 Gaps: 3

US-09-854-562-2 (1-83) x US-09-777-347-1 (1-564)

Qy 1 MetAlaArgSerIleTyRPhMeAlaPheLeuValIleuAla---ThrLeuPheValAla 19
Db 40 ATGGCTGCTTCATTTCTTCATGSCATTTTGCTTGGCAATATGCTCTTTGTTACC 99

Qy 20 TyrGlyValGlnGlyLeuGluLeuLeuCys---CysLysGluLeuThrLysProValLysCys 38
Db 100 TATGAGTAGAAGCAGCAGCAAAATTGCAAGACCAAGCAAACTTCCAGCATTAATCT 159

Qy 39 SerSerAppProLeuCyseGlnLysLeuCyseMetGlnLysGluLysTyRGlusAspGlyHis 58
Db 160 TTTATGACTCATCATCTAGAGAAATATGTATC---AAAGAGAAATTATCTGCTGAGACAT 216

Qy 59 CysPheThrIleLeuSerLysCyseLysCysMetLysAsnLysGlyAsnAlaLysThrIleuAla 78
Db 217 TGTAGCAAACTCCAAAGAGAGTGTATGCTATGCACTAAGCATGTATTTGACAAATCTCA 276

Qy 79 ThrGluLeuAla 83
Db 277 AGTGAAAGTTAAAGCA 291

RESULT 2
US-09-777-347-2
Sequence 2, Application US/09777347
Patent No. US20010014977A1
GENERAL INFORMATION:
APPLICANT: McBride, Kevin E.
Scalder, David M.
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/777,347
FILING DATE: 05-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,087
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 07/554,195
FILING DATE: 17-JUL-90
APPLICATION NUMBER: USSN 07/382,518
FILING DATE: 19-JUL-89
ATTORNEY/AGENT INFORMATION:
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 91-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2
US-09-777-347-2

Alignment Scores:
Pred. No.: 2,22e-08 Length: 3528
Score: 132.00 Matches: 42
Percent Similarity: 33.33% Conservative: 11
Best Local Similarity: 26.42% Mismatches: 29
Query Match: 29.66% Indels: 77
DB: 9 Gaps: 4

US-09-854-562-2 (1-83) x US-09-777-347-2 (1-3528)

Qy 1 MetAlaArgSerIleTyRPhMeAlaPheLeuValIleuAla---ThrLeuPheValAla 19
Db 2638 ATGGCTGCTTCATTTCTTCATGSCATTTTGCTTGGCAATATGCTCTTTGTTACC 2697

Qy 20 TyrGlyValGlnGlyLeuGluLeuLeuCys---CysLysGluLeuThrLysProValLysCys 38
Db 2698 TATGCTTTCCTCATATTATTCCTCTAAATCATCGCAATPAAAAAATGTAACG 2757

Qy 25 LysGluLeuLeuCyseLysGluLeuThrLysProValLysCys 37
Db 2758 AAGCAGACATCATGTAACCGTTTAATTAACCTTAAAAAATGTAATGATTAATCTT 2817

Qy 37 37
Db 2818 GCTATACGTTTAACAACATATGATAAAAAAACCCTAAATATCTATTGCGTCT 2877

Qy 37 37
Db 2878 CTCTCATGTTATTTCTAATATTTTGTGTGATGATGATGAGGTAGAGCTCAGCA 2937

Qy 38 38
Db 2938 AATTGCAAGACCAAGCAAACTTCCAGCATTAATGTTTATGAGATCATCATGTAG 2997

Qy 45 nLysLeuCyseMetGlnLysGluLysTyRGlusAspGlyHisCysPheThrIleuSerLys 65
Db 2998 AAAATATTTATC---AAAGAGAAATTTACTGCTGAGCATTTGTAGCAAACTCCAAAGAA 3054

Qy 65 sCysLeuCyseMetLysAsnLysGlyAsnAlaLysThrIleuAlaThrGluLeuAla 83
Db 3055 GTGCTATGCACTAAGCATGTATTTGACAAATCTCAAGTGAAGTTAAAGCA 3109

RESULT 3

```

GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Harvell, Leslie
APPLICANT: Cahoon, Rebecca
APPLICANT: McCutchen, Billy Fred
APPLICANT: Lu, Albert
APPLICANT: Herrmann, Rafael
APPLICANT: Wong, James
TITLE OF INVENTION: Defensin Polynucleotides and Methods of
FILE REFERENCE: 35718/246703
CURRENT APPLICATION NUMBER: US/10/178,213
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/300,152
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ. ID NOS: 459
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 295
LENGTH: 307
TYPE: DNA
ORGANISM: Hedera helix
FEATURE:
NAME/KEY: CDS
LOCATION: (3) ... (158)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (3) ... (140)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 263, 270, 285, 294, 301, 306
OTHER INFORMATION: n = A,T,C or G
US-10-178-213-295

Alignment Scores:
Pred. No.:
Score: 0.000469 Length: 307
Percent Similarity: 91.50 Matches: 17
Best local Similarity: 57.89% Conservative: 5
Query Match: 44.74% Mismatches: 15
DB: 20.56% Indels: 1
Gaps: 14
US-09-854-562-2 (1-83) x US-10-178-213-295 (1-307)

Cy 38 CysSerSerArgProLeuCyGlnGlySerLeuCyMetClnGlySerGlnGlySerTyrGluAspGly 57
Db 39 TGACCGAGTATGCGACAGTGTAAAGAACTTTGC--GAGAAAGATGATGATCTTTTGATGCT 95
Cy 58 HieCySPheThrIleLeuSerIysCySLeuCyMetIysArgCyAsnAlaIys 75
Db 96 CACTGCGTCGCGCTTATTACAAAATGTATTGCGCGCTGGAATTGTCCGCCAAA 149

RESULT 5
US-10-178-213-412
Sequence 412, Application US/10178213
Publication No. US20030041348A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Harvell, Leslie
APPLICANT: Cahoon, Rebecca
APPLICANT: McCutchen, Billy Fred
APPLICANT: Lu, Albert
APPLICANT: Herrmann, Rafael
APPLICANT: Wong, James
TITLE OF INVENTION: Defensin Polynucleotides and Methods of
FILE REFERENCE: 35718/246703
CURRENT APPLICATION NUMBER: US/10/178,213
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/300,152

```

```

RESULT 6
US-10-178-213-124
Sequence 124, Application US/10178213
Publication No. US20030041348A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Harvell, Leslie
APPLICANT: Canoun, Rebecca
APPLICANT: McCutchen, Billy Fred
APPLICANT: Lu, Albert
APPLICANT: Herrmann, Rafael
APPLICANT: Wong, James
TITLE OF INVENTION: Defensein Polynucleotides and Methods of
TITLE OF INVENTION: Use
FILE REFERENCE: 35718/246703
CURRENT APPLICATION NUMBER: US/10/178,213
CURRENT FILING DATE: 2002-06-21
PRIORITY APPLICATION NUMBER: 60/300,152
PRIORITY FILING DATE: 2001-06-22
PRIORITY APPLICATION NUMBER: 60/300,241
PRIORITY FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 124

```

```

; TYPE: DNA
; ORGANISM: Momordica charantia
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (71)..(265)
;
; FEATURE:

```

```
; NAME/KEY: mat_peptide
; LOCATION: (107) ... (262)
US-10-178-213-121
```

Alignment Scores:

Pred. No.:	0.00268	Length:	36
Score:	87.00	Matches:	25
Percent Similarity:	40.45%	Conservative:	11
Best Local Similarity:	28.09%	Mismatches:	43
Query Match:	19.55%	Indels:	10
DB:	14	Gaps:	2

US-09-854-562-2 (1-83) x US-10-178-213-121 (1-367)

Qy	2	Ala	Arg	Ser	Ile	Leu	Thr	Met	Ala	Phe	Leu	Val	Ile	Ala	Thr	Leu	Phe	Val	Ile	Arg	Gly	21	
	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::		
Db	53	TCC	CA	TGC	AG	CTG	TTC	TTC	GA	TTC	CTC	CC	CTT	CTC	CTT	GC	AT	G	GA	AT	G	CA	112
Qy	22	Val	Gln	Gly	Leu	Glu	Leu	Cys	Val	Glu	Leu	Thr	Leu	Pro	Val	Leu	Cys	Ser	Ser	Asp	41		
	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::		
Db	113	TGT	AGG	G	G	G	GA	CA	TGC	CA	GTG	GA	AG	CA	CC	AT	CG	AT	TTC	CA	TGC	AT	172
Qy	42	Pro	Leu	Cys	Gln	Leu	Cys	Met	Glu	Gly	Gly	Leu	Ala	Phe	Gly	His	Cys	Phe	Thr	61			
	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::			
Db	173	CAC	ACT	GTC	CA	AG	ACT	TGT	---	CGA	AA	CGA	AG	CTT	AT	CCG	G	TGC	CA	CTG	GA	222	
Qy	62	Ile	Leu	Ser	Leu	Cys	Leu	Cys	Met	Leu	Arg	Cys	---	---	---	---	---	---	---	---	72		
	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::			
Db	230	TTT	TGC	CGC	GCT	GTT	TTC	G	CA	TAA	AGC	CTG	TAC	TAG	CTT	GAT	GAT	CA	TAT	ATC	288		
Qy	73	Asp	Ala	Leu	Thr	Leu	Ala	Thr	Glu	Leu	81												
	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::												
Db	290	AAT	G	CA	AAT	AT	TC	AT	G	CA	ACT	TTT	TTA	316									

RESULT 8
US-09-87

```

: Sequence 10791, Application US/09878574
: Patent No. US20020110548A1
: GENERAL INFORMATION:
: APPLICANT: Byrum, Joseph R.
: APPLICANT: La Rosa, Thomas J.
: APPLICANT: Thompson, Michael D.
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
: TITLE OF INVENTION: Plants
: FILE REFERENCE: 38-21(15401)B
: CURRENT APPLICATION NUMBER: US/09/878,574
: CURRENT FILING DATE: 2001-12-21
: PRIOR APPLICATION NUMBER: 09/333,535
: PRIOR FILING DATE: 1999-06-14
: NUMBER OF SEQ ID NOS: 15775
: SEQ ID NO 10791
: LENGTH: 272
: TYPE: DNA
: ORGANISM: Glycine max
: OTHER INFORMATION: Clone ID: 700968067H1
US-09-878-574-10791

```

Alignment Scores:

Pred. No.:	0.00207	length:	27
Score:	86.50	Matches:	12
Percent Similarity:	45.00%	Conservative:	24
Best Local Similarity:	30.00%	Mismatches:	35
Query Match:	19.44%	Indels:	9
DB:	10	Gaps:	4

US-09-854-562-2 (1-83) x US-09-878-574-10791 (1-272)

```

QY      1 MetalaaGserIleTYrPheMetAla---PheLeuValLeuAlaThrLeuPheValAla 19
      2 .....
Db      29 ATGTCGCGCTCGGCGCCCTTGGTTCACCACTTTTCCTTGGCTTCGCTTCGCGGCC 88
      30 .....
QY      20 TyrGlyValGlnGlyLysGlnIle-----CysCysLysGlnLeuThrLys 34
      21 .....

```

Db 89 ACTGAGATGATGGGCCAACATGTTGGCAGAGCAGAACTTGTGAGTCTCAGAGCCAC 148

35 ProValLys-----CysSerSerAspProLeuCysGlnLysLeuCysMetGluGlu 52

Db 149 CGTTTCAAGGGCCATGTTGAGTGACACCAACTGTGGCTCTGTTTGC --CGAACCGAA 205

ay : 53 LYSTYRG1UASPRG1YH1SCysphethr1leUserLySCysleuCysmetLySargCys 72

Db 206 CGTTTCACTGAGGACACTGCCGTGGCTTCCGTCCGAGATGCTTCTGCACCAACAATTGT 265

RESULT 9

```

US-09-878-574-11794
; Sequence 11794, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878, 574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333, 535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 11794
; LENGTH: 277
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701064907H1
US-09-878-574-11794

```

Alignment Scores:

Pred. No.:	0.00212	Length:	27
Score:	86.50	Matches:	19
Percent Similarity:	45.95%	Conservative:	15
Best Local Similarity:	25.68%	Mismatches:	37
Query Match:	19.44%	Indels:	2
DB:	10	Gaps:	2

US-09-854-562-2 (1-83) X US-09-878-574-11794 (1-277)

OY	I	MechAArgSerIleTyPhemetalapheneValIleuAlatThrLeuPheValAlaTyr	20
	::::	::::	::::
Db	51	TTCGTTCCACCAATTTCTCTGTCTTCGTCTTGCGGCACACGAGCATGATGGGCCCA	110
	::::	::::	::::
OY	21	GlyValGlnGlyAsnIleCysCysLysGlnLeuThrLysProValIys-----Cys	38
	::::	::::	::::
Db	111	ACAATGTTGGCACAAAGCAAAGAACTGTAGTCTCAGACCACCGTTTAAGGGCCATGT	176
	::::	::::	::::
OY	39	SerSerAspProLeuCysGlnLysIleuCyMetGluLysTyrGluAspGlyHis	58
		::::	:::::
Db	171	TTGAGTGACACCAACTGTGGCTCTGTATTGC---CGAACCGAAACGTTTCATCGAGGACAC	227
	::::	::::	::::
OY	59	CysPheThrIleuLeuSerLysCysLeuCyMetLysAlaGlyCys	72
	::::	::::	::::
Db	228	TGCCTGGCTTCCTCGTCGACGAATGCTTCTGCACCAACAATTGT	269

OTHER INFORMATION: n = A, T, C or G

Percent Similarity: 42.50%

```

Length: 466
Matches: 23
Conservative: 11
Mismatch: 38

```


FILE REFERENCE: 35/18/246/03
CURRENT APPLICATION NUMBER: US/10/178,213
CURRENT FILING DATE: 2002-06-21

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic acid search, using frame_plus_p2n model

Run on: August 23, 2003, 07:03:33 ; Search time 1918 Seconds
(without alignments)
1051.758 Million cell updates/sec

Title: US-09-854-562-2
Perfect score: 445
Sequence: 1 MARSIFYMAFLVATLTFVAY.....SKCLCMKKNKATLATELLA 83

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame.p2n.model -DEV=xlh
-O=/cgn2.1/USPTO/US09854562/runat_22082003_103830_4817/app_query.fasta_1.263
-DB=BST -QFMT=fastp -SUFIX=p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=txt -NORM=ext -HSA PSI=500 -MINLEN=0 -MAXLEN=2000000000
-USER=U09854562@cgn2.1 2135 @runat_22082003_103830_4817 -NCPU=6 -ICPU=3
-NO MMAP -LARGEBUFFER -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:
1: em_estba.*
2: em_estchum.*
3: em_estlin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	434.5	97.6	448 12	BM063616	BM063616 KS01057E0
2	434.5	97.6	506 14	CB164889	CB164889 KS050143T
3	427.5	96.1	416 14	CB164909	CB164909 KS050169T
4	427.5	96.1	633 14	CB164987	CB164987 KS0600583
5	425.5	95.6	332 14	CB164858	CB164858 KS050090T
6	425.5	95.6	527 12	BM064680	BM064680 KS01070A0
7	425.5	95.6	648 14	CB185066	CB185066 KS04236T7
8	425.5	95.5	530 12	BM062133	BM062133 KS01038H0
9	422.5	94.9	496 14	CB164824	CB164824 KS050003T
10	421.5	94.7	720 14	CB185076	CB185076 KS04192T7
11	329.5	74.0	231 9	AF082706	AF082706 AF082706
12	329.5	74.0	521 14	CA524161	CA524161 KS12033G0
13	329.5	74.0	535 12	BM062737	BM062737 KS01046F0
14	329.5	74.0	540 12	BM063527	BM063527 KS01056D1
15	329.5	74.0	545 14	CA525505	CA525505 KS12056G0
16	329.5	74.0	580 12	BM065064	BM065064 KS01074E1
17	318.5	71.6	474 14	CA525605	CA525605 KS12058F0
18	309	69.4	339 12	BM060748	BM060748 KS01018B0
19	309	69.4	447 14	CA524497	CA524497 KS12038D0
20	309	69.4	466 12	BM063884	BM063884 KS01060F0
21	309	69.4	474 14	CA514352	CA514352 KS09023C0
22	309	69.4	481 12	BM064296	BM064296 KS01065D0
23	309	69.4	509 12	BM061371	BM061371 KS01029G1
24	309	69.4	522 12	BM064663	BM064663 KS01069H0
25	309	69.4	532 12	BM063609	BM063609 KS01057D1
26	309	69.4	537 12	BM064540	BM064540 KS01068D0
27	309	69.4	571 14	CA515865	CA515865 KS09048E1
28	308	69.2	306 14	CA517625	CA517625 KS09086E0
29	304	68.3	337 14	CA514064	CA514064 KS09016E1
30	302	67.9	380 12	CA514462	CA514462 KS09025A0
31	298	67.0	376 12	BM062401	BM062401 KS01042C0
32	262	58.9	318 14	CA516127	CA516127 KS09053F0
33	237.5	53.4	500 12	BM061668	BM061668 KS01033C1
34	223	50.1	536 12	BM063253	BM063253 KS01053C0
35	217.5	48.9	513 12	BM063138	BM063138 KS01052A0
36	217.5	48.9	574 12	BM067544	BM067544 KS08007B0
37	217.5	48.9	672 12	BM064987	BM064987 KS01073F0
38	203.5	45.7	573 14	CA523446	CA523446 KS12022C1
39	185.5	41.7	419 9	AM399651	AM399651 EST10151
40	185.5	41.7	421 9	AM399675	AM399675 EST10151
41	183.5	41.2	207 12	BM059656	BM059656 KS01003B0
42	182.5	41.0	333 9	AM623112	AM623112 EST121057
43	182.5	41.0	378 9	AM487824	AM487824 EST246146
44	182.5	41.0	477 9	AM897392	AM897392 EST266835
45	182.5	41.0	480 9	AM490243	AM490243 EST248569

ALIGNMENTS

RESULT 1
BM063616
LOCUS BM063616 448 bp mRNA linear EST 11-SEP-2002
DEFINITION KS01057E08 KS01 Capsicum annuum cDNA, mRNA sequence.
ACCESSION BM063616
VERSION BM063616.1 GI:22783734
KEYWORDS EST.
SOURCE Capsicum annuum
ORGANISM Capsicum annuum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Capsicum.
REFERENCE 1 (bases 1 to 448)

AUTHORS Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S., Hur, C.-G., and Choi, D.
TITLE Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annuum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen
JOURNAL Unpublished
COMMENT Contact: Doil Choi
 Genome Research Center and National Center for Genome Information
 Korea Research Institute of Biotechnology and Biotechnology
 P.O. Box 115, Yusong, Taejeon, 305-600, Republic of Korea
 Tel: 82-42-860-4340
 Fax: 82-42-860-4309
 Email: doil@mail.kribb.re.kr
 High quality sequence stop: 448.
 Location/Qualifiers

FEATURES

source
 1..448
 /organism="Capsicum annuum"
 /mol_type="mRNA"
 /cultivar="Bukang"
 /db_xref="taxon:4072"
 /cruise_type="leaf inoculated with Xanthomonas campestris pv. glycines"
 /dev_stage="8 weeks after germination"
 /clone_lib="KS01"
 /note="Vector: pBluescript SK(-)"

BASE COUNT 165 a 67 c 84 g 132 t
ORIGIN

Alignment Scores:
 Pred. No.: 3,86e-45 Length: 448
 Score: 434.50 Matches: 83
 Percent Similarity: 98.81% Conservative: 0
 Best Local Similarity: 98.81% Mismatches: 0
 Query Match: 97.64% Indels: 1
 DB: 12 Gaps: 1

US-09-854-562-2 (1-83) x BM063616 (1-448)

QY 1 MetalaargserietleTyPhemecalaphleuValleuA1a---ThrlaupheVala1a 19
DB 54 ATGGCTCGTTCATTACTTCATGCGCATTTCTTGTCGCAATGACCCCTTGTTGCT 113
QY 20 TyrglYvalGInglysgulileCyCyblysgulueThrylryProvallylryCysser 39
DB 114 TATGGGCTGCAGGCAAGAAATTTGCTGTAAGAGCTCCAAACCTGTAATGTTCT 173
QY 40 SerAaPProleuCyGlnlyleuCySmelGulysGulueThrylryGluaspGlyh1aCys 59
DB 174 AGTGACCTCTATGTCAAAACCTGTAAGAGAGAAATATGAGATGATGCTATTGT 233
QY 60 PheThrlleuSerlylryCySmelGulysGulueThrylryGluaspGlyh1aCys 79
DB 234 TTCACATCTTAAGCAAGTCTTATGATGATGATGATGATGATGATGATGATGATGAT 293
QY 80 GluleuLeuA1a 83
DB 294 GAATGCTTGCT 305

RESULT 2
CB164889 506 bp mRNA linear EST 30-JAN-2003
LOCUS CB164889
DEFINITION KS05014370 KS05 Capsicum annuum cDNA, mRNA sequence.
ACCESSION CB164889.
VERSION CB164889.1 GI:28151015
KEYWORDS EST.
SOURCE Capsicum annuum
ORGANISM Capsicum annuum
 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Capsicum.

REFERENCE Lee, S.-J., Lee, M.-Y., Lee, P.-S., Choi, S.-H. and Harn, C.-H.
AUTHORS EST fragments generated by SSH of SIRO red- SBV red
TITLE

JOURNAL Unpublished
COMMENT Contact: Chee Hark Harn
 Biotechnology center
 NONG WOO BIO CO., LTD.
 537-17 Jeondan, Gnam, Yeosu, Kyonggi 469-885, Republic of Korea
 Tel: 82 31 883 7055
 Fax: 82 31 884 7065
 Email: chharn@nongwoobio.co.kr
 Seq primer: 77.
 Location/Qualifiers

FEATURES

source
 1..506
 /organism="Capsicum annuum"
 /mol_type="mRNA"
 /cultivar="SIRO, SBV"
 /db_xref="taxon:4072"
 /sex="hermaphrodite"
 /tissue_type="fruit"
 /dev_stage="mature red"
 /clone_lib="KS05"
 /note="Vector: pGEM-T easy; Site 1: EcoRI; SIRO red - SBV red suppression subtractive cDNA library of Hot pepper. The subtraction was performed using the PCR-select cDNA subtraction kit (Clontech, Palo Alto, CA) according to the manufacturer's instructions. For a tester, cDNA from HR-developing pepper leaves sampled after 3 days inoculation was synthesized using AMV reverse transcriptase while, for a driver, cDNA from noninoculated pepper leaves was synthesized. After the subtractive hybridization, the subtracted cDNAs are selectively amplified by using nested PCR primers to enrich differentially expressed sequences."

BASE COUNT 154 a 82 c 101 g 169 t
ORIGIN

Alignment Scores:
 Pred. No.: 4.54e-45 Length: 506
 Score: 434.50 Matches: 83
 Percent Similarity: 98.81% Conservative: 0
 Best Local Similarity: 98.81% Mismatches: 0
 Query Match: 97.64% Indels: 1
 DB: 14 Gaps: 1

US-09-854-562-2 (1-83) x CB164889 (1-506)

QY 1 MetalaargserietleTyPhemecalaphleuValleuA1a---ThrlaupheVala1a 19
DB 72 ATGGCTCGTTCATTACTTCATGCGCATTTCTTGTCGCAATGACCCCTTGTTGCT 131
QY 20 TyrglYvalGInglysgulileCyCyblysgulueThrylryProvallylryCysser 39
DB 132 TATGGGCTGCAGGCAAGAAATTTGCTGTAAGAGCTCCAAACCTGTAATGTTCT 191
QY 40 SerAaPProleuCyGlnlyleuCySmelGulysGulueThrylryGluaspGlyh1aCys 59
DB 192 AGTGACCTCTATGTCAAAACCTGTAAGAGAGAAATATGAGATGATGATGATGAT 251
QY 60 PheThrlleuSerlylryCySmelGulysGulueThrylryGluaspGlyh1aCys 79
DB 252 TTCACATCTTAAGCAAGTCTTATGATGATGATGATGATGATGATGATGATGATGAT 311
QY 80 GluleuLeuA1a 83
DB 312 GAATGCTTGCT 323

RESULT 3
CB164909 416 bp mRNA linear EST 30-JAN-2003
LOCUS CB164909
DEFINITION KS05016970 KS05 Capsicum annuum cDNA, mRNA sequence.
ACCESSION CB164909
VERSION CB164909.1 GI:28151035
KEYWORDS EST.
SOURCE Capsicum annuum
ORGANISM Capsicum annuum

Db 323 GAATTCCTGCT 334

RESULT 5
CBI64858 332 bp mRNA linear EST 30-JAN-2003
DEFINITION K050090T0 K505 Capsicum annuum cDNA, mRNA sequence.
ACCESSION CBI64858
VERSION CBI64858.1 GI:28150984
KEYWORDS EST.
SOURCE Capsicum annuum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Capsicum.
1 (bases 1 to 332)
REFERENCE Lee, S.-J., Lee, M.-Y., Lee, P.-S., Choi, S.-H. and Han, C.-H.
EST fragments generated by SSH of SIRO red- SBV red
AUTHORS
TITLE
JOURNAL
COMMENT Unpublished
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Biotechnology Center
NONG WO BIO CO., LTD.
537-17 Jeongdan, Ganam, Yeosu, Jeonnam, 550-705, Republic of Korea
Tel: 82 31 883 7055
Fax: 82 31 884 7065
Email: chharn@nongwoobio.co.kr
Seq primer: 17.
Location/Qualifiers
1..332
/organism="Capsicum annuum"
/mol_type="mRNA"
/cultivar="SIRO, SBV"
/db_xref="taxon:4072"
/sex="hermaphrodite"
/tissue_type="Fruit"
/dev_stage="mature red"
/clone_idb="KS05"
/note="Vector: pGEM-T easy; Site 1: EcoRI, SIRO red - SBV red suppression subtractive cDNA library of Hot pepper. The subtraction was performed using the PCR-select cDNA subtraction kit (Clontech, Palo Alto, CA) according to the manufacturer's instructions. For a tester, cDNA from HR-developing pepper leaves sampled after 3 days inoculation was synthesized using AMV reverse transcriptase while, for a driver, cDNA from noninoculated pepper leaves was synthesized. After the subtractive hybridization, the subtracted cDNAs are selectively amplified by using nested PCR primers to enrich differentially expressed sequences."

BASE COUNT 96 a 59 c 69 g 108 t
ORIGIN

Alignment Scores:
Pred. No.: 3 62e-44 Length: 332
Score: 425.50 Matches: 81
Percent Similarity: 97.59% Conservative: 0
Best Local Similarity: 97.59% Mismatches: 1
Query Match: 95.62% Indels: 1
DB: 15 Gaps: 1

US-09-854-562-2 (1-83) x CBI64858 (1-332)

QY 1 MetAlaArgSerIleTyrPheMetAlaPheLeuValLeuAla---ThrLeuPheValAla 19
DB 78 ATGGCTCGTTCATTACTTCATGCGCATTTCTGCTTGCGCAATGACCTCTTGTTGCT 137
QY 20 TyrGlyValGlnGlyLysGluIleCysGlyGlnLeuThrLysProValLysCysSer 39
DB 138 TATGGGGTGCAGGCAAGAAATTCTGTAAAGACTCACCAAAACCTGTAAATGTTCT 197
QY 40 SerAspProLeuCysGlnLysLeuCysMetGlnLysGlnLysTyrGlnAspGlyHisCys 59
DB 198 AGTGAACCTCTATGTCAAAAACCTGTATGAGAGAGAAATATATGAATGCTCATTTGT 257

QY 60 PheThrIleLeuSerLysCysLeuCysMetLysArgCysAsnAlaLysThrLeuAlaThr 79
DB 258 TTCACATCTTAAGAGATGCTTATGATGAGAGATGTAATGCTTAACCTTGCAACA 317
QY 80 GlnLeuLeu 82
DB 318 GAATTCCTT 326

RESULT 6
BM064680 527 bp mRNA linear EST 11-SEP-2002
LOCUS BM064680
DEFINITION K01070A06 K501 Capsicum annuum cDNA, mRNA sequence.
ACCESSION BM064680
VERSION BM064680.1 GI:22784798
KEYWORDS EST.
SOURCE Capsicum annuum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Capsicum.
1 (bases 1 to 527)
REFERENCE Lee, S.-J., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S., Hur, C.-G. and Choi, D.
Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annuum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen
JOURNAL Unpublished
CONTACT: Doil Choi
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P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
Tel: 82-42-860-4340
Fax: 82-42-860-4309
Email: doil@mail.kribb.re.kr
High quality sequence stop: 527.
Location/Qualifiers
1..527
/organism="Capsicum annuum"
/mol_type="mRNA"
/cultivar="Bukang"
/db_xref="taxon:4072"
/tissue_type="leaf inoculated with Xanthomonas campestris pv. glycines"
/dev_stage="8 weeks after germination"
/clone_idb="KS01"
/note="Vector: pBluescript SK(-)"

BASE COUNT 175 a 74 c 100 g 178 t
ORIGIN

Alignment Scores:
Pred. No.: 6.69e-44 Length: 527
Score: 425.50 Matches: 81
Percent Similarity: 97.59% Conservative: 0
Best Local Similarity: 95.58% Mismatches: 1
Query Match: 95.62% Indels: 1
DB: 12 Gaps: 1

US-09-854-562-2 (1-83) x BM064680 (1-527)

QY 1 MetAlaArgSerIleTyrPheMetAlaPheLeuValLeuAla---ThrLeuPheValAla 19
DB 31 ATGGCTCGTTCATTACTTCATGCGCATTTCTGCTTGCGCAATGACCTCTTGTTGCT 90
QY 20 TyrGlyValGlnGlyLysGluIleCysGlyGlnLeuThrLysProValLysCysSer 39
DB 91 TATGGGGTGCAGGCAAGAAATTCTGTAAAGACTCACCAAAACCTGTAAATGTTCT 150
QY 40 SerAspProLeuCysGlnLysLeuCysMetGlnLysGlnLysTyrGlnAspGlyHisCys 59
DB 151 AGTGAACCTCTATGTCAAAAACCTGTATGAGAGAGAAATATATGAATGCTCATTTGT 210
QY 60 PheThrIleLeuSerLysCysLeuCysMetLysArgCysAsnAlaLysThrLeuAlaThr 79

DB 211 TTCAACATCTTCAAGGAGAGCTTATGCTATGACAGATGATATGCTATTAACCTTCCACACA 270

QY 80 GlnLeuLeu 82

DB 271 GAACGCTT 279

RESULT 7

LOCUS CB185066

DEFINITION KS04236T70 KS04 Capsicum chinense cDNA, mRNA sequence.

ACCESSION CB185066

VERSION CB185066.1 GI:28197055

KEYWORDS EST.

SOURCE Capsicum chinense

ORGANISM Capsicum chinense

REFERENCE 1 (bases 1 to 648)

AUTHORS Lee,S.J., Lee,M.Y., Choi,S.H., Her,N.H., Yang,S.G. and Harn,C.H.

TITLE Generation of Expressed Sequence Tags from Hot Pepper (Capsicum chinense) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen

JOURNAL Unpublished

COMMENT Contact: Chee Hark Harn

Biotechnology center

NONG WOO BIO CO., LTD.

537-17 Jeongdan, Ganam, Yeoju, Kyonggi 469-885, Republic of Korea

Tel: 82 31 883 7055

Fax: 82 31 884 7065

Email: chharn@nongwoobio.co.kr

Seq primer: 77.

FEATURES

source

1..648

location/Qualifiers

/organism="Capsicum chinense"

/mol_type="mRNA"

/cultivar="P1257284"

/db_xref="taxon:80379"

/sex="thermaphrodite"

/tissue_type="leaf"

/dev_stage="7-8 weeks-old leaves"

/clone_idb="KS04"

/note="Vector: pGEM-T easy; Site 1: EcoRI; PMW-induced suppression subtractive cDNA library of hot pepper. The subtraction was performed using the PCR-select cDNA subtraction kit (Clontech, Palo Alto, CA) according to the manufacturer's instructions. For a tester, cDNA from HR-developing pepper leaves sampled after 3 days inoculation was synthesized using AMV reverse transcriptase while, for a driver, cDNA from noninoculated pepper leaves was synthesized. After the subtractive hybridization, the subtracted cDNAs are selectively amplified by using nested PCR primers to enrich differentially expressed sequences."

BASE COUNT 197 a 115 c 132 g 196 t 8 others

ORIGIN

Alignment Scores:

Pred. No.: 8,82e-44 Length: 648

Score: 425.50 Matches: 82

Percent Similarity: 97.62% Conservative: 0

Best Local Similarity: 97.62% Mismatches: 1

Query Match: 95.62% Indels: 1

DB: 14 Gaps: 1

US-09-854-562-2 (1-83) x CB185066 (1-648)

QY 1 MetalAaRGSerIleTyrPheMetIaPheLeuValIleuAla---ThrIleuPheValAla 19

DB 132 ATGGCTCCTTCATTACTTCAAGCATTCTTCTGCTTGCGACATGACACTCTTTGTTGCC 191

QY 20 TyrGlyValaGlnGlyLeuIleCysCysLeysGlnLeuThrLysPProValIleCysSer 39

Dd					
Oy	192	AATGGGCTGCACAGCAAGAAATTTCGTGTAAAGACTTCAAAAACCCTTTAATGTTCT	251		
Oy	40	SerAspProLeuCysGlnIlyLeuCYsmetGluYsgIuYstyrgIuaepgIyhS Cys	59		
Dd	252	AGGACCCCTCTATGTCAA AAAA CTCTGTATGGAGAAGGAATAATGAAGATGTCATGT	311		
Oy	60	PheThrTlleUenSerLyCysLeuCYsmeLYsarGYSaenaAlalytHrLenuAlthr	79		
Dd	312	TTCACAATCCTTAAGCAMAGTGCTTATGTCATGAAGATATATATGCTAAAACTTCGCAACA	371		
Oy	80	GluLeuLeuAla	83		
Dd	372	GAATGCTTGTCT	383		
RESULT 8 BM062133					
LOCUS		BM062133	530 bp	mRNA	linear EST 11-SEP-2000
DEFINITION		KS01038H06 KS01 Capsicum annuum cDNA, mRNA sequence.			
ACCESSION		BM062133			
VERSION		BM062133.1			
KEYWORDS		GI:22782251			
SOURCE		EST.			
ORGANISM		Capsicum annuum			
		Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta			
		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
		asterids; lamiales; Solanales; Solanaceae; Capsicum.			
		1e.S., Kim,S.-Y., Chung,Y.-H., Shin,H.-J., Goh,S.-H., Pai,H.-S.,			
		Huh,C.-G. and Choi,D			
		Generation of Expressed Sequence Tags from Hot Pepper (Capsicum			
		annum L.) and Sequence Analysis in Relation to Hypersensitive			
		Response Against Pathogen			
		Unpublished			
JOURNAL		Contact: Dool Choi			
COMMENT		Genome Research Center and National Center for Genome Information			
		Korea Research Institute of Bioscience and Biotechnology			
		P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea			
		Tel: 82-42-860-4340			
		Fax: 82-42-860-4309			
		Email: doil@mail.krdb.re.kr			
		High quality sequence stop: 530.			
FEATURES		Location/Qualifiers			
source		1..530			
		/organism="Capsicum annuum"			
		/mol_type="mRNA"			
		/culivar="Bukang"			
		/db_xref="taxon:4072"			
		/tissue_type="leaf inoculated with Xanthomonas campestris			
		p.v. glycines"			
		/dev_stage="8 weeks after germination"			
		/clone_lib="KS01"			
		/note="Vector: pBluescript SK(-)"			
BASE COUNT	176 a	76 c	99 g	175 t	
ORIGIN					
Alignment Scores:					
Pred. No.:	7,81e-44	Length:	530		
Score:	425.00	Matches:	83		
Best Similarity:	97.65%	Conservative:	0		
Percent local Similarity:	97.65%	Mismatches:	0		
Query Match:	95,51%	Indels:	2		
DB:	12	Gaps:	0		
US-09-854-562-2 (1-83) x BM062133 (1-530)					
Oy	1	MethAlarGserLleTyrrHeMecaLaPheuValleuala--ThrieuPheValalAt	20		
Dd	34	ATGGCTCGTCCATTACTTCAATGCCATTTCTTGCTGGCATGACCTCTTGTGCTT	93		
Oy	20	yrgIyaIeIngIylvsygIIecYSySvSGluLeuThrlYseProvalYscysSers	40		
Dd	94	ATGGGAGGCAAGCAAGAAATTTGCTGMAAGACCTCAAAAACCTGTMAATGTTCTA	153		

Qy	40	erAspProLeucCys61InyLysuCy5m6tGluYv5GluYvTYGluYvSpGlyHisCysP	60
Db	154	GTGACCCCTCTATGTCAAAACTCTGTATGAGAGAGAGAAATATGAAATGTCATTGTT	213
Qy	60	hehThiLeuSerLysCysLeuCy5m6tLysvGlyvAsnAlaLysThrLeuAlaThrg	80
Db	214	TCACATCTCTAAGCAAGAGCTTATCATGAAGATGAATGCTAAACTCTCCACAG	273
Qy	80	IuleuLeuAla	83
Db	274	AATTGCTTGCT	284
RESULT 9			
LOCUS	CB164824	496 bp	linear
DEFINITION	KS050003T0 KS05 Capsicum annuum CDNA, mRNA sequence.		EST 30-JAN-2003
VERSION	CB164824		
ACCESSION	CB164824.1		GI:28150950
KEYWORDS	EST.		
SOURCE	Capsicum annuum		
ORGANISM	Capsicum annuum		
REFERENCE	Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; Lamiales; Solanales; Solanaceae; Capsicum.		
AUTHORS	Lee,S.-J., Lee,M.-Y., Lee,P.-S., Choi,S.-H. and Hahn,C.H.		
TITLE	EST fragments generated by SSH of SIRO red- SBV red		
JOURNAL	Unpublished		
COMMENT	Contact: Chee Hark Harn Biotechnology Center NONG WO0 BIO CO.,LTD. 537-17 Jeongdan, Ganam, Yeoju, Kyonggi 469-885, Republic of Korea Tel: 82 31 883 7055 Fax: 82 31 884 7065 Email: chharn@nongwoobio.co.kr Seq primer: 17.		
FEATURES			
source	location/Qualifiers		
	1..496		
	/organism="Capsicum annuum"		
	/mol_type="mRNA"		
	/cultivar="SIRO, SBV"		
	/db_xref="taxon:4072"		
	/sex="hermaphrodite"		
	/tissue.type="fruit"		
	/dev stage="mature red"		
	/clone_id="KS05"		
	/note="Vector: pGEM-T easy; Site 1: EcoRI; SIRO red- SBV red suppression subtractive cDNA library of Hot pepper. The subtraction was performed using the PCR-select cDNA subtraction kit (Clontech, Palo Alto, CA) according to the manufacturer's instructions. For a tester, cDNA from HR-developing pepper leaves sampled after 3 days inoculation was synthesized using AMV reverse transcriptase while, for a driver, cDNA from noninoculated pepper leaves was synthesized. After the subtractive hybridization, the subtracted cDNAs are selectively amplified by using nested PCR primers to enrich differentially expressed sequences."		
BASE COUNT	155 a	77 c	99 g
ORIGIN	165 t		
Alignment Scores:			
Pred. No.:	1,496-43	Length:	496
Score:	422.50	Matches:	80
Percent Similarity:	97.58%	Conservative:	1
Best Local Similarity:	96.35%	Mismatch:	1
Query Match:	94.94%	Indels:	1
DB:	14	Gaps:	1
US-09-854-562-2 (1-83) x CB164824 (1-496)			
Qy	1	MetalaArgSerLysTyrPheMetAlaPheLeuValLeuAla	--ThrLeuPheValAla 19

Accession	Source	Organism	Reference Authors	Journal Comment	Features
Dp	ATGGCTGCTTCATTTACTTCATGAGCATTTCTTGCTTGCCAAATGACACTTGTGCT	128			
Oy	20 TyGClYalalInglYlYsgIuIlcYsCYsYlYsgIuIleuhtlYsProlYlYsCYsSer	39			
Dp	129 TATGGGGTGTGAAGCAAGAAATTTGCTGTAAAGAGCTCAAAAACCTGTTAAATGTCT	188			
Oy	40 SerAsProlYlYsCYsGlnYlYsLeuCYsMetGlnYlYsGlnYlYsTYrgIuAaPglYhIsCYs	59			
Dp	189 AGTACACCTCTATGTCAAAAACCTGTGATGTAGAGAGAGAAATATGAAGATGGTCATGTT	248			
Oy	60 PhehtlYlYsYlYsCYsLeuCYsMetYlYsYlYsCYsAsnAlYlYshtlYlYsAlaThr	79			
Dp	249 TACCAATCTCTAAGAGAGAGCTTATGATCATGAAGAGATGATGCTAAACCTTGCAACA	308			
Oy	80 GluIleuYlYs	82			
Dp	309 GAATTGCTT	317			
RESULT 10					
LOCUS	CB185076	720 bp	mRNA	linear	EST 03-FEB-2003
DEFINITION	KS041922T10 KS04 Capsicum chinense CDNA, mRNA sequence.				
ACCESSION	CB185076				
VERSION	CB185076.1	GI:28197069			
KEYWORDS	EST.				
SOURCE	Capsicum chinense				
ORGANISM	Capsicum chinense				
REFERENCE	Bukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Capsicum.				
AUTHORS	Lee,S.-J., Lee,M.-Y., Choi,S.H., Her,N.H., Yang,S.G. and Harn,C.H.				
TITLE	Generation of Expressed Sequence Tags from Hot pepper(Capsicum chinense) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen				
JOURNAL	Unpublished				
COMMENT	Contact: Chee Hark Harn Biotechnology center NONG WOONG BIO CO., LTD. 537-17 Joongdan, Ganam, Yeuju, Kyonggi 469-885, Republic of Korea Tel: 82 31 883 7055 Fax: 82 31 884 7065 Email: chharn@nongwoobio.co.kr Seq primer: T7.				
FEATURES	Location/Qualifiers				
SOURCE	1..720				
	/organism="Capsicum chinense"				
	/mol_type="mRNA"				
	/cultivar="PI257284"				
	/db_xref="taxon:80379"				
	/sex="thermaphrodite"				
	/tissue_type="leaf"				
	/dev_stage="7-8 weeks-old leaves"				
	/clone_id="KS04"				
	/note="Vector: pGEM-T easy; Site_1: EcoRI; PMW-induced suppression subtractive cDNA library of Hot pepper. The subtraction was performed using the PCR-select cDNA subtraction kit (Clontech, Palo Alto, CA) according to the manufacturer's instructions. For a tester, cDNA from HR-developing pepper leaves sampled after 3 days inoculation was synthesized using AMV reverse transcriptase while, for a driver, cDNA from noninoculated pepper leaves was synthesized. After the subtractive hybridization, the subtracted cDNAs are selectively amplified by using nested PCR primers to enrich differentially expressed sequences."				
BASE COUNT	203 a	114 c	133 g	218 t	52 others
ORIGIN					
Alignment Scores:	3,28e-43	Length:	720		
Pred. No.:	421.50	Matches:	81		
Score:					

Percent Similarity: 97.59%
 Best Local Similarity: 97.59%
 Query Match: 94.72%
 DB: 14 Gaps: 1

US-09-854-562-2 (1-83) x CB185076 (1-720)

QY 1 MetAlaAGSerIleTyPheMetAlaPheLeuValIleuAla---ThrluPheValAla 19
 DB 200 ATGGCTCGTTCATTACTTCAATGCAATTTCTTGCTTGCGCAATGACACTCTTTGTTGCC 259
 QY 20 TyrgIyValGInGlyLysGluIleCyCsYsGlyGluLeuThrluPheProValIyScYsSer 39
 DB 260 AATGGGGGCAAGCAAGCAAGAAATTTGCTGTAAAGAGCTCACAAAACCTGTTAAATGTTCT 319
 QY 40 SerAaPProLeuCyGInLysLeuCySmetGluLysGluLysTyrgIuAspGlyHisCys 59
 DB 320 AGTGACCTCTATGTCAAAACTGTGTATGAGAAAGCAAAATATGAAGATGTCATTGT 379
 QY 60 PheThrlleuSerIleTyPheMetAlaPheLeuValIleuAlaThr 79
 DB 380 TTCAACAATCTTAAAGAGTCTTATGATGAGAGATGTATGCTAAACTCTCCGACACA 439
 QY 80 GluLeuLeu 82
 DB 440 GAATTGCTN 448

RESULT 11

LOCUS AF082706 231 bp mRNA linear EST 27-MAR-2000
 DEFINITION AF082706 Capsicum annuum leaf mRNA Capsicum annuum cDNA clone 12
 similar to gamma-thionin-like protein, mRNA sequence.

ACCESSION AF082706
 VERSION AF082706.1 GI:3462809
 KEYWORDS EST.
 SOURCE Capsicum annuum
 ORGANISM Capsicum annuum

JOURNAL Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Capsicum.
 REFERENCE 1 (bases 1 to 231)
 Jung, H.W. and Hwang, B.K.
 Isolation, partial sequencing, and expression of
 pathogenesis-related cDNA genes from pepper leaves infected by
 Xanthomonas campestris pv. vesicatoria

JOURNAL M01. Plant Microbe Interact. 13 (1), 136-142 (2000)
 MEDLINE 20120389
 PUBMED 10656596
 COMMENT Contact: Byung Kook Hwang
 Department of Agricultural Biology
 Korea University
 Anam-dong, Sungbuk-gu, Seoul 136-701, Korea
 Email: bkwang@kuicn.korea.ac.kr.

FEATURES

source 1..231
 location/Qualifiers
 /organism="Capsicum annuum"
 /mol_type="mRNA"
 /cultivar="Handyu1"
 /db_xref="taxon:4072"
 /clone="12"
 /tissue_type="leaf"
 /clone_1ib="Capsicum annuum leaf mRNA"

BASE COUNT 70 a 38 c 45 g 78 t
 ORIGIN

Alignment Scores:
 Pred. No.: 3.7e-32 Length: 231
 Score: 329.50 Matches: 63
 Percent Similarity: 98.44% Conservative: 0
 Best Local Similarity: 98.44% Mismatches: 0
 Query Match: 74.04% Indels: 1
 DB: 9 Gaps: 1

US-09-854-562-2 (1-83) x AF082706 (1-231)

QY 1 MetAlaAGSerIleTyPheMetAlaPheLeuValIleuAla---ThrluPheValAla 19
 DB 40 ATGGCTCGTTCATTACTTCAATGCAATTTCTTGCTTGCGCAATGACACTCTTTGTTGCT 99
 QY 20 TyrgIyValGInGlyLysGluIleCyCsYsGlyGluLeuThrluPheProValIyScYsSer 39
 DB 100 TATGGGGGCAAGCAAGCAAGAAATTTGCTGTAAAGAGCTCACAAAACCTGTTAAATGTTCT 159
 QY 40 SerAaPProLeuCyGInLysLeuCySmetGluLysGluLysTyrgIuAspGlyHisCys 59
 DB 160 AGTGACCTCTATGTCAAAACTGTGTATGAGAAAGCAAAATATGAAGATGTCATTGT 219
 QY 60 PheThrlleuLeu 63
 DB 220 TTCACAATCTTA 231

RESULT 12

LOCUS CA524161 521 bp mRNA linear EST 15-NOV-2002
 DEFINITION KS12033G04 KS12 Capsicum annuum cDNA, mRNA sequence.

ACCESSION CA524161
 VERSION CA524161.1 GI:25038231
 KEYWORDS EST.
 SOURCE Capsicum annuum
 ORGANISM Capsicum annuum

JOURNAL Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Capsicum.
 REFERENCE 1 (bases 1 to 521)
 Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S.,
 Hur, C.-G. and Choi, D.
 Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
 annuum L.) and Sequence Analysis in Relation to Hypersensitive
 Response Against Pathogen

JOURNAL Unpublished
 COMMENT Contact: Doil Choi
 Genome Research Center and National Center for Genome Information
 Korea Research Institute of Bioscience and Biotechnology
 P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
 Tel.: 82-42-860-4340
 Fax: 82-42-860-4309
 Email: doil@mail.kribb.re.kr
 Plate: 033 row: G column: 04.

FEATURES

source 1..521
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 /mol_type="mRNA"
 /db_xref="taxon:4072"
 /clone_1ib="KS12"

BASE COUNT 163 a 77 c 101 g 180 t
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 Score: 329.50 Matches: 63
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 Best Local Similarity: 71.59% Mismatches: 8
 Query Match: 74.04% Indels: 5
 DB: 14 Gaps: 2

US-09-854-562-2 (1-83) x CA524161 (1-521)

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 DB 56 ATGGCTCGTTCATTACTTCAATGCAATTTCTTGCTTGCGCAATGACACTCTTTGTTGCC 115
 QY 20 TyrgIyValGInGlyLysGluIleCyCsYsGlyGluLeuThrluPheProValIyScYsSer 39
 DB 116 AATGAGGTGCAAGCAAGCAAGAAATTTGCTGTAAAGATGCTCAAGAGCTGTATATATGTTCT 175
 QY 40 SerAaPProLeuCyGInLysLeuCySmetGluLysGluLysTyrgIuAspGlyHisCys 59

D	b		176	AGTACCCGGCTATGTCACAACAAATCTGTATTAAAGGAGCAACTAATGAATGCTATTGT	235
Oy			60	PheThrIleLeuSerLysCysLeuCysMetLysAlaCysAsn-----AlaLys	75
D	b		236	TTCACAAATCTCTAAGGAGATGGCGTATGCATGAAGAGATGTAATGTGTTACAGATGTAA	295
Oy			76	ThrlenuAlathrGluleuLeuAla	83
D	b		296	ACTCTGCCAGCAAATTTGCTTGCT	319
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RESULT 13					
BM062737					
LOCUS			BM062737	535 bp	mRNA linear EST 11-SEP-2002
DEFINITION			KS01046F09 KS01 Capsicum annuum cDNA,		mRNA sequence.
ACCESSION			BM062737		
VERSION			BM062737.1		GI:22782855
KEYWORDS			EST.		
SOURCE			Capsicum annuum		
ORGANISM			Capsicum annuum		
REFERENCE			Eukaryota; Vitidipiantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Capsicum.		
AUTHORS			Lee,S.-Y.,Kim,S.-Y., Chung,Y.-H., Shin,H.-J., Goh,S.-H., Pai,H.-S., Hur,C.-G. and Choi,D.		
TITLE			Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen		
JOURNAL COMMENT			Unpublished		
			Contact: Doil Choi		
			Genome Research Center and National Center for Genome Information		
			Korea Research Institute of Bioscience and Biotechnology		
			P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea		
			Tel: 82-42-860-4340		
			Fax: 82-42-860-4309		
			Email: doil@mail.kribb.re.kr		
FEATURES			High quality sequence stop: 535.		
source			Location/Qualifiers		
			1..535		
			/organism="Capsicum annuum"		
			/mol_type="mRNA"		
			/culivar="Bukang"		
			/db_xref="taxon:4072"		
			/tissue_type="leaf inoculated with Xanthomonas campestris pv. glycines"		
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			/note="Vector: pBluescript SK(-)"		
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ORIGIN			177 t		
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Pred. No.:			1,136-31	Length:	535
Score:			329.50	Matches:	63
Percent Similarity:			85.23%	Conservative:	12
Best Local Similarity:			71.59%	Mismatches:	8
Query Match:			74.04%	Indels:	5
DB:			12	Gaps:	2
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Oy			1	MetaLaarGerSerIleTerPheMetaIaPheLeuValLeuAla---	ThrlenuPheValAla 19
D	b		33	ATGGTGCTTCATTCATTACTTCATGSCATTTCTGTGCTTGCGCATGACCCTCTTTGTC	92
Oy			20	TyrGlyValGInglyLysGluLeuCysCysLysGluLeuThrLysProValLysCysSer	39
D	b		93	AATGAGTGCAAGGATGAAGAAATTTGCTGTAAAGATGCTCAAGAGCTGTATAATGTTCT	152
Oy			40	SerAspProLeuCysGlnLysLeuLeuCysMetGlyLysGluLysTyrgluAspGlyHisCys	59
D	b		153	AGTAGCCCGCATGTAAACAAATTCGTATCGAAGGAGGAACATAAGAAGATGTCATTGT	212

Qy	60	PhehrilleuserylsCysLeuCYeMetLysArgCysAsn-----AlaLys	75
Db	213	TTTCACATCCCTACAGAACTGCGTATGCATGAGAGATGTATGTGTTGACAGATCTTAA	272
Qy	76	ThrLeuAlaThrGluLeuLeuAla	83
Db	273	ACTCTGCGAGCAAAATGCTTGCT	296
RESULT 14			
EM063527	BM063527	540 bp	mRNA linear EST 11-SEP-2007
LOCUS	KS01056D12	KS01 Capsicum annuum cDNA, mRNA sequence.	
DEFINITION	BM063527		
ACCESSION	BM063527.1	GI:22783645	
VERSION	EST.		
KEYWORDS	Capsicum annuum		
SOURCE	Capsicum annuum		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Capsicum.		
REFERENCE	1 (bases 1 to 540)		
AUTHORS	Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S., Hur, C.-G. and Choi, D.		
TITLE	Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annuum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen		
JOURNAL	Unpublished		
COMMENT	Contact: Doil Choi Genome Research Center and National Center for Genome Information Korea Research Institute of Bioscience and Biotechnology P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea Tel: 82-42-860-4340 Fax: 82-42-860-4309 Email: doil@mail.kr.rib.re.kr High quality sequence stop: 540.		
FEATURES	Location/Qualifiers		
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	/mol_type="mRNA"		
	/cultivar="Bukang"		
	/db_xref="taxon:4072"		
	/tissue_type="leaf inoculated with Xanthomonas campestris pv. glycines"		
	/dev_stage="8 weeks after germination"		
	/clone_lib="KS01"		
	/note="Vector: pBluescript SK(-)"		
BASE COUNT	185 a 77 c 103 g 175 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	1.15e-31	Length:	540
Score:	329.50	Matches:	63
Percent Similarity:	85.23%	Conservative:	12
Best Local Similarity:	71.59%	Mismatches:	8
Query Match:	74.04%	Indels:	5
DB:	12	Gaps:	2
US-09-854-562-2 (1-83) x BM063527 (1-540)			
Qy	1	MetaLaarSeriLleYrPheMeLaAlaPheLeuValLeuAla---ThrLeuPheValAla	19
Db	39	ATGCGTGGTTCATCTTACTTCATGCGCAATTCCTTGCTTGGCAAGACCCCTCTTTGTTGCC	98
Qy	20	TyrGlyValGlnGlyLysGluLeuCYeLysGluLeuThrLysProValLysCysSer	39
Db	99	AATGAGGGGCAAGGTAAAGAAATTTGCTGTAAGAGTGTCTCAAGAGCGCTTATATGTTCT	158
Qy	40	SerAspProLeuCYeGlnLysLeuCYeMetGluLysGluLysTyrGluAspGlyHisCYe	59
Db	159	AGTACCCCGCATGTCAACAAATGTGTATTAAAGAGGAACATGAAAGATGGTCATTGT	218
Qy	60	PheThrIleuSerLysCYeLeuCYeMetLysArgCysAsn-----AlaLys	75

Search completed: August 23, 2003, 08:18:05
Job time : 1920 secs

Db 219 TTCACATCTTACAGAGAGGCTATGACATGACGACATGTAATGCTGTCAGAGTGTAA 278
QY 76 ThrLeuAlaThrGluLeuLeuAla 83
Db 279 ACTCTGCGACGCAAAATTGCTTGT 302

RESULT 15

CA525505 545 bp mRNA linear EST 15-NOV-2002
LOCUS KS12056G07 KS12 Capsicum annuum cDNA, mRNA sequence.

DEFINITION CA525505
ACCESSION CA525505.1 GI:25039585

VERSION
KEYWORDS
SOURCE

ORGANISM Capsicum annuum

Capiscum annuum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Capsicum.

REFERENCE

1 (bases 1 to 545)
Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S.,
Hur, C.-G. and Choi, D.

Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
annuum L.) and Sequence Analysis in Relation to Hypersensitive
Response Against Pathogen

JOURNAL

CONTACT: Doil Choi
Genome Research Center and National Center for Genome Information
Korea Research Institute of Bioscience and Biotechnology
P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea

Tel: 82-42-860-4340
Fax: 82-42-860-4309
Email: doil@mail.kribb.re.kr
Plate: 056 row: G column: 07.

FEATURES

Location/Qualifiers
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/organism="Capsicum annuum"
/mol_type="mRNA"
/db_xref="taxon:4072"
/clone_lib="KS12"

BASE COUNT 182 a 84 c 106 g 173 t
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Pred. No.: 1,166-31 Length: 545
Score: 329.50 Matches: 63
Percent Similarity: 85.23% Conservative: 12
Best Local Similarity: 71.59% Mismatches: 8
Query Match: 74.04% Indels: 5
DB: 14 Gaps: 2

US-09-854-562-2 (1-83) x CA525505 (1-545)

QY 1 MetAlaArgSerIleTyrPheMetAlaPheLeuValLeuAla---ThrLeuPheValAla 19
Db 50 ATGGGCTCGTTCATTACTTCAATGGATTCTGCTTGSCAATGACCTCTTGTGGC 109
QY 20 TyrGlyValGlnGlyLysGluIleCysCysLysGluLeuThrLysProValLysCysSer 39
Db 110 AATGAGGTGCAGAGTAAGGAAATTGCTGTAAAGATGCTCAAGAGCTGTATATGTTCT 169
QY 40 SerAaPProLeuCysGlnLysLeuCysMetGluLysGluLysTyrGluAspGlyHisCys 59
Db 170 AATGACCCGCGATATGTAACAATCTGATCGAAGAGAGAACTATGAGATGATGTCATTGT 229
QY 60 PheThrIleLeuSerLysCysLeuCysMetLysArgCysAsn-----AlaLys 75
Db 230 TTCACATCTTACAGAGAGGCGATATGCAATGATGATGATGATGATGATGATGATGATGAT 289
QY 76 ThrLeuAlaThrGluLeuLeuAla 83
Db 290 ACTCTGCGACGCAAAATTGCTTGT 313

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model.

Run on: August 22, 2003, 06:31:08 ; Search time 2024 Seconds

(without alignments)
1677.618 Million cell updates/sec

Title: US-09-854-562-2

Sequence: 1 MARSIVMFLVLTFLVAV.....SKLCIMRCNAKTLATLLELLA 83

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
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21: em_or:*
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39: em_hcgo_hum:*
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41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	434.5	97.6	506	8 AF112443	AF112443 Capsicum
2	431.5	97.0	548	8 AF112869	AF112869 Capsicum
3	234	52.6	559	8 AF128239	AF128239 Capsicum
4	189.5	42.6	558	8 AB005266	AB005266 Nicotiana
5	188	42.2	601	8 AF509566	AF509566 Nicotiana
6	186	41.8	589	8 SFSTRNA	Z11748 Solanaceae
7	182.5	41.0	596	8 SLU20591	U20591 Solanum lyc
8	177.5	39.9	549	8 AB005250	AB005250 Nicotiana
9	156	35.1	448	8 AB005265	AB005265 Nicotiana
10	130.5	29.3	456	8 AF507975	AF507975 Petunia x
11	129	29.0	602	8 AF507976	AF507976 Petunia x
12	129	21.2	470	8 ST322R	X13180 Petalio mRNA
13	94.5	20.3	139934	8 AP003272	AP003272 Oryza sat
14	90.5	20.3	139934	8 AP003246	AP003246 Oryza sat
15	89	20.0	382	8 AB052687	AB052687 Pyrus pyr
16	88.5	19.9	242507	2 AC134246	AC134246 Mus muscu
17	87.5	19.7	177202	2 AC118703	AC118703 Mus muscu
18	87	19.6	401	8 AB052689	AB052689 Pyrus pyr
19	87	19.6	181376	2 AC114990	AC114990 Mus muscu
20	87	19.6	238725	2 AC130214	AC130214 Mus muscu
21	86.5	19.4	527	8 GMI12150	U2150 Glycine max
22	84.5	19.0	403	8 OSU72942	U72942 Oryza sativ
23	84.5	19.0	458	8 AB052688	AB052688 Pyrus pyr
24	84.5	19.0	63748	8 AP000604	AP000604 Arabidops
25	84	18.9	594	6 AR085469	AR085469 Sequence
26	84	18.9	594	6 AR170812	AR170812 Sequence
27	84	18.9	594	6 I36742	I36742 Sequence 1
28	84	18.9	109155	8 ATT20K12	AL137898 Arabidops
29	83.5	18.8	71239	2 AC099903	AC099903 Mus muscu
30	83.5	18.8	112106	9 AC105142	AC105142 Homo sapi
31	83.5	18.8	167153	2 AC132088	AC132088 Mus muscu
32	83.5	18.8	178544	10 AC124557	AC124557 Mus muscu
33	83.5	18.8	179115	9 AP004710	AP004710 Homo sapi
34	83	18.7	2608	10 AF373288	AF373288 Mus muscu
35	83	18.7	171287	2 AC131115	AC131115 Mus muscu
36	83	18.7	204986	2 AC127581	AC127581 Mus muscu
37	82.5	18.5	169463	2 AC127006	AC127006 Rattus no
38	82.5	18.5	255654	2 AC107481	AC107481 Rattus no
39	82	18.4	54022	8 AP004901	AP004901 Lotus jap
40	82	18.4	186095	4 AC091505	AC091505 Sus scrof
41	82	18.4	241740	2 AC111892	AC111892 Rattus no
42	82	18.4	261110	2 AC105842	AC105842 Rattus no
43	82	18.4	263108	2 AC112034	AC112034 Rattus no
44	81	18.2	234	6 AX505923	AX505923 Sequence
45	81	18.2	234	8 BT004647	BT004647 Arabidops

RESULT 1

ALIGNMENTS

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 DEFINITION AF112443
 ACCESSION AF112443
 VERSION AF112443.1 GI:6552501
 KEYWORDS
 SOURCE Capsicum annuum
 ORGANISM Capsicum annuum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamids; Solanales; Solanaceae; Capsicum.
 REFERENCE 1 (bases 1 to 506)
 AUTHORS Oh,B.J., Ko,M.K., Kostenyuk,I., Shin,B. and Kim,K.S.
 TITLE Coexpression of a defensin gene and a thionin-like gene via different signal transduction pathways in pepper and Colletotrichum gloeosporioides interactions
 JOURNAL Plant Mol. Biol. 41 (3), 313-319 (1999)
 MEDLINE 20064969
 PUBMED 10598099
 REFERENCE 2 (bases 1 to 506)
 AUTHORS Oh,B.J., Ko,M.K., Kostenyuk,I.A., Shin,B.C. and Kim,K.S.
 TITLE Direct Submission
 JOURNAL Submitted (09-DEC-1998) Kumho Life and Environmental Science Laboratory, Kumho Petrochemical Co., LTD., 1 Oryong-dong, Puk-gu, Kwangju 500-712, Korea
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 Best local Similarity: 98.81% Mismatches: 10
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 Db 10 ATGGCTGCTTCATTTACTTCTCATGSCATTTCTTGCTTGGAAGACCCCTTTGTTGCT 69
 Oy 20 TyrGlyValGlnGlyLysGlnIleCysCysLysGlnLeuThrLysProValLysCysSer 39
 Db 70 TATGGGGTGAAGCAAGCAAGAAATTGCTGTAAGAGCTCAAAAACCTGTAATGTTCT 129
 Oy 40 SerAspProLeuCySGlnLysLeuCyMetGlnLysGlnLysTyrGlnAspGlyHisCys 59
 Db 130 AGTGACCTCTATGTCAAAACCTCTGTATGAGAGGAAGAAATATGAAGAGTGCTATGCT 189
 Oy PheThrIleLeuSerLysCysLeuCyMetLysAspGlyAsnAlaLysThrLeuAlaThr 79
 Db 190 TTCACATCTTAAGCAAGAGTCTATGATGAAGAGATTAATGCTAAACCTGCAACA 249
 Oy 80 GluLeuLeuAla 83
 Db 250 GAATTGCTTGGCT 261

RESULT 2
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 LOCUS Capsicum annuum gamma-thionin 1 precursor (thion1) mRNA, complete cds.
 DEFINITION AF112869
 ACCESSION AF112869
 VERSION AF112869.1 GI:6601330
 KEYWORDS
 SOURCE Capsicum annuum
 ORGANISM Capsicum annuum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamids; Solanales; Solanaceae; Capsicum.
 REFERENCE 1 (bases 1 to 548)
 AUTHORS Hwang,B.K., Lee,S.C., Kim,Y.J. and Hong,J.K.
 TITLE Molecular cloning and pathogen-induced expression of a thionin gene in pepper plant
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 548)
 AUTHORS Hwang,B.K., Lee,S.C., Kim,Y.J. and Hong,J.K.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-1998) Dept. of Agricultural Biology, Korea University, Anam-dong, Sungbuk-gu, Seoul 136-701, Korea
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 BASE COUNT 186 a 76 c 107 g 179 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 8,98e-46 Length: 548
 Score: 431.50 Matches: 82
 Percent Similarity: 98.81% Conservative: 1
 Best local Similarity: 97.62% Mismatches: 0
 Query Match: 96.97% Indels: 1
 DB: 8 Gaps: 1
 US-09-854-562-2 (1-83) x AF112869 (1-548)
 Oy 1 MetAlaArgSerIleTyrPheMetAlaPheLeuValIleuAla---ThrLeuPheValAla 19
 Db 52 ATGGCTGCTTCATTTACTTCTCATGSCATTTCTTGCTTGGAAGACCCCTTTGTTGCT 111
 Oy 20 TyrGlyValGlnGlyLysGlnIleCysCysLysGlnLeuThrLysProValLysCysSer 39
 Db 112 TATGGGGTGAAGCAAGCAAGAAATTGCTGTAAGAGCTCAAAAACCTGTAATGTTCT 171
 Oy 40 SerAspProLeuCySGlnLysLeuCyMetGlnLysGlnLysTyrGlnAspGlyHisCys 59
 Db 172 AGTGACCTCTATGTCAAAACCTCTGTATGAGAGGAAGAAATATGAAGAGTGCTATGCT 231
 Oy PheThrIleLeuSerLysCysLeuCyMetLysAspGlyAsnAlaLysThrLeuAlaThr 79

QY	73	-----AsnAlaIysThrLeuAlaThrGluLeuLeu	82
Db	279	CCTAATGATGTGGACATAATTTGGTTCAGGATGCTCTAAACTTCGAAACAGACAAATGCTT	338
RESULT 4			
AB005266			
LOCUS	AB005266	558 bp	linear
DEFINITION	Nicotiana excelsior mRNA for gamma-thionin, complete cds.		
ACCESSION	AB005266		
VERSION	AB005266.1	GI:2244704	
KEYWORDS	gamma-thionin.		
SOURCE	Nicotiana excelsior		
ORGANISM	Nicotiana excelsior		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Asteridiales; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Lamiales; Solanales; Solanaceae; Nicotiana.		
AUTHORS	1 (sites)		
TITLE	Yamada,S., Komori,T. and Imaeeki,H.		
JOURNAL	CDNA Cloning of gamma-thionin from Nicotiana excelsior (Accession No. AB005266) (PGR97-131)		
REFERENCE	Plant Physiol. 115, 314 (1997)		
AUTHORS	2 (bases 1 to 558)		
TITLE	Yamada,S.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (26-JUN-1997) Shigehiro Yamada, Plant Breeding and Genetics Research Laboratory, Japan Tobacco Inc., 700 Higashibara, Iwata, Shizuoka 438, Japan		
AUTHORS	(E-mail:shigehiro.yamada@pbgrl.jti.co.jp, Tel.0538-32-7116, Fax:0538-32-8700)		
FEATURES	Location/Qualifiers		
source	1..558		
gene	/organism="Nicotiana excelsior"		
CDs	/mol_type="mRNA"		
	/db_xref="taxon:61185"		
	1..558		
	/gene="Nethio2"		
	33..350		
	/gene="Nethio2"		
	/codon_start=1		
	/product="gamma-thionin"		
	/protein_id="BAA21114.1"		
	/db_xref="GI:2244705"		
	/translation="MARSCVFMAFAIAYMLFVAAYDVADKCKTESNTPGICITKPECRKCIKEKFTDGHCSKILRCLCTKPCVDEKMIKTGAETLAEEATTLAAALEEETMDN"		
BASE COUNT	170 a 94 c 108 g 186 t		
ORIGIN			
Alignment Scores:			
Pred. NO.:	6.97e-15	Length:	558
Score:	189.50	Matches:	43
Percent Similarity:	60.00%	Conservative:	11
Best Local Similarity:	47.78%	Mismatches:	25
Query Match:	42.58%	Indels:	11
	8	Gaps:	3
US-09-854-562-2 (1-83) x	AB005266 (1-558)		
QY	1	MetAlaArgSerIleTyrrPheMetAlaPheLeuValLeuAlaThr--LeuPheValAla	19
Db	33	ATGCTCGCTCCGATGCTTCATGATGCAATTCCTTGGAGAGATGCTCTTGTTC	92
QY	20	TyrGlyValGlnGlyLysGluIleCysCysLysGluLeuThrLysProValLysCysSer	39
Db	93	TATGATGTGGAGCTAAAGATTGCCAAAACAGAAAGCAATATCTCCCTCGAATATGCA	152
QY	40	SeAspProLeuCySGlnLysLeuCyMetGluLysGluLysGlyTyrgluAspGlyHisCys	59
Db	153	ACCAAAACACATCAGAAAAGCTTGATC--AAAGAGAAATTTACTGATGTCATTTGT	209
QY	60	PheThrIleLeuSerLysCysLeuCyMetLysArgCys-----	72

Db	210	AGCAAAATCTTCAGGAAGGTCTAAGCACTAAGCATGTCGTGTGATGAGAAATGATC	269
QY	73	-----AsnAlaIysThrlenuAlaThrGlu 80	
Db	270	AAACAGGAGCTGAAACTTACTGATGAGA 299	
RESULT 5			
AF509566			
LOCUS			
DEFINITION	AF509566	601 bp	mRNA linear
ACCESSION	Nicotiana alata flower-specific defensin precursor (Nad1) mRNA,		
VERSION	complete cds.		
KEYWORDS	AF509566.1 GI:25005096		
SOURCE			
ORGANISM	Nicotiana alata (Persian tobacco)		
REFERENCE	Nicotiana alata		
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamids; Solanales; Solanaceae; Nicotiana.		
TITLE	1 (bases 1 to 601)		
JOURNAL	Lay, F.T., Schirra, H.J., Scanlon, M.J., Anderson, M.A. and Craik, D.J.		
MEDLINE	The three-dimensional solution structure of Nad1, a new floral defensin from Nicotiana alata and its application to a homology model of the crop defense protein alfAFP		
PMID	J. Mol. Biol. 325 (1), 175-188 (2003)		
REFERENCE	12473460		
AUTHORS	2 (bases 1 to 601)		
TITLE	Lay, F.T., Brugliera, F. and Anderson, M.A.		
JOURNAL	Isolation and Properties of Floral Defensins from Ornamental Tobacco and Petunia		
PMID	Plant Physiol. 131 (3), 1283-1293 (2003)		
REFERENCE	12644678		
AUTHORS	3 (bases 1 to 601)		
TITLE	Lay, F.T. and Anderson, M.A.		
JOURNAL	Direct Submission		
PMID	Submitted (06-MAY-2002) Biochemistry, La Trobe University,		
REFERENCE	Bundoora, VIC 3086, Australia		
AUTHORS	Location/Qualifiers		
TITLE	1. .601		
JOURNAL	/organism="Nicotiana alata"		
PMID	/mol_type="mRNA"		
REFERENCE	/db_xref="taxon:4087"		
AUTHORS	1. .601		
TITLE	/gene="Nad1"		
JOURNAL	61. .378		
PMID	/gene="Nad1"		
REFERENCE	/note="Nad1, gamma-thionin; possesses antifungal activity		
AUTHORS	targeted to the vacuole"		
TITLE	/codon_start=1		
JOURNAL	/product="flower-specific defensin precursor"		
PMID	/protein_id="AA070999.1"		
REFERENCE	/db_xref="GI:25005097"		
AUTHORS	/translation="MARSLICFWAFAILAMLFVAYEVOAREKTESNTPGICITKPKP		
TITLE	CRKAIISKEFTDGHCSKILRLRLCTKPKPCVPERHMKTGAEILAEAKTLAALALEEB		
JOURNAL	MDN"		
PMID	136. .276		
REFERENCE	/gene="Nad1"		
AUTHORS	/product="flower-specific defensin"		
TITLE	BASE COUNT 192 a 95 c 115 g 199 t		
JOURNAL	ORIGIN		
PMID	mat_peptide		
REFERENCE			
AUTHORS	Alignment Scores:		
TITLE	Pred. No.:	1.17e-14	Length:
JOURNAL	Score:	188.00	Matches:
PMID	Percent Similarity:	54.55%	Conservative:
REFERENCE	Best Local Similarity:	45.45%	Mismatches:
AUTHORS	Query Match:	42.25%	Indels:
TITLE	DB:	8	Gaps:
JOURNAL			3
PMID	US-09-854-562-2 (1-83) x AF509566 (1-601)		
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PMID			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PMID			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PMID			
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TITLE			
JOURNAL			
PMID			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PMID			
REFERENCE			
AUTHORS			
TITLE			

Db	61	ATGGCTGGCTCTCTTGTCCTTCATCGCATTTGGCTATCTTGGCAATGATGCTCTTGTGGCC	120
Qy	20	TyrglyValGlnGlyLeuGluIleCysCysIysGluLeuThrIlyProValIysCysSer	39
Db	121	TATAGAGTCAGACGCTAAGATGCAAAACAGAAAGCAACACATTTCTGTGAATATGCAATT	180
Qy	40	SerAspProLeuCysGlnIlyLeuCysMetGlnIlyIysTyrgIyAspGlyHisCys	59
Db	181	ACCAACACCATCAGAGAAAGCTTGATC---AGTAGAAATTACTGATGTCATTTGT	237
Qy	60	PhenThrIleuSerIysCysLeuCysMetIysArgCys-----	72
Db	238	AGCAAAATTCCTCAGAAAGTGGCTATGTAACGACCATGTGTGTTGATGAGAAATGACT	297
Qy	73	-----AsnAlaIysThrIleuAlaThrGluLeuLeu	82
Db	298	AAAACAGAGCTGAAATTTTGCTGCTGAGAGCAAAACATTTGGCTGCAGCTTGGCTT	354
RESULT 6			
LOCUS	SFSTPMNA	589 bp	mRNA linear PLN 03-DEC-1993
DEFINITION	Solanaaceae mRNA for flower-specific thionin.		
ACCESSION	Z11748	S41631	
VERSION	Z11748.1	GI:21212	
KEYWORDS	thionin.		
SOURCE	Solanaaceae		
ORGANISM	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Asteridae; Lamiales; Magnoliophyta; eudicotyledons; core eudicots; Solanales.		
REFERENCE	1 (bases 1 to 589)		
AUTHORS	Gu,Q., Kawata,E.E., Morse,M.J., Wu,H.M. and Cheung,A.Y.		
JOURNAL	A flower-specific cDNA encoding a novel thionin in tobacco		
MEDLINE	Mol. Gen. Genet. 234 (1), 89-96 (1992)		
PUBMED	92357021		
REFERENCE	2 (bases 1 to 589)		
AUTHORS	Gu,Q.		
TITLE	Direct Submission		
JOURNAL	Submitted (25-FEB-1992) Qing GU, Department of Biology, Yale University, 165 Prospect St, New Haven, CT, 06511, USA		
FEATURES	Location/Qualifiers		
source	1..589		
	/organism="Solanaaceae"		
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	/clone="49A"		
	/tissue_type="flower of tobacco"		
	/dev_stage="flowering"		
	49..366		
	/codon_start=1		
	/product="flower-specific thionin"		
	/protein_id="CAA7806.1"		
	/db_xref="GI:21213"		
	/db_xref="SWISS-PROT:P32026"		
	/translation="MARSLCFMAFALIAAMLPAVYEQVQAECKTESVTPGICITKPP		
	CRACISEKFTDGCSTLRRLCTCPVDEDMIKIGAEITLVEAEKTLAALLBESI		
	MDN"		
BASE COUNT	184 a	97 c	114 g 194 t
ORIGIN			
Alignment Scores:			
Pred. No.:	2.06e-14	Length:	589
Score:	186.00	Matches:	44
Percent Similarity:	54.55%	Conservative:	10
Best Local Similarity:	44.44%	Mismatches:	27
Query Match:	41.80%	Indels:	18
DB:	8	Gaps:	3
Qy	US-09-854-562-2 (1-83) x SFSTPMNA (1-589)		
	1 MetAlaArgSerIleTyrrPheMetAlaPheLeuValLeuAla---ThrIleuPheValAla 19		


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Db 49 ATGGCTGCTCTTCTGCTTCATGCAATTCTCTATCTTGGCAATGAGCTGTTTGCC 108
Qy 20 TyrglyValGlnGlyLysGlnIleCysGlySgluLeuThrLysProValLysCysSer 39
Db 109 TATAGGCTGCAAGCTGATGAGATGCAAAACAGAAATATATGCAATT 168
Qy 40 SerAspProLeuCysGlnLysLeuCysMetGluLysGlnLysTyrglyLysPglYHisCys 59
Db 169 ACCAAACCATCATGACAGAAAGCTTGATC--AGTGAATATTACTGATGTCATTTGT 225
Qy 60 PheThrIleLeuSerLysCysLeuCysMetLysArgCys----- 72
Db 226 AGCAAACTCCTCAGACGGTGCCTATGCACTAAGCCATGCTGTTGATGAGAAGATGATA 285
Qy 73 -----AsnAlaIysThrLeuAlaThrGluLeu 82
Db 286 AAAACAGAGCTGAACCTTGTGTTGAGAGCAAAACCTTGGCTGCAGCTTTGCTT 342

RESULT 7
LOCUS SU020591 596 bp mRNA linear PLN 04-NOV-1995
DEFINITION Solanum lycopersicum flower-specific gamma-thionin-like
protein/acidic protein precursor, mRNA, complete cds.
VERSION U20591
KEYWORDS U20591.1 GI:924623
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 596)
Mulligan,S.B. and Gasser,C.S.
Nature and regulation of pistil1-expressed genes in tomato
Plant Mol. Biol. 28 (4), 691-711 (1995)
JOURNAL MEDLINE 95375233
PUBMED 7647301
REFERENCE 2 (bases 1 to 596)
AUTHORS Mulligan,S.B.
TITLE Direct Submission
SUBMITTED (02-FEB-1995) Stephen B. Mulligan, Molecular and Cellular
Biology, University of California at Davis, Davis, CA 95616, USA.
FEATURES
Source
1..596
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/strain="VP36"
/db_xref="taxon:4081"
/clone="TPP3"
/tissue_type="pistil1"
/clone_lib="lambda gt10 library from Gasser lab"
/dev_stage="immature"
1..56
57..374
/codon_start=1
/product="flower-specific gamma-thionin-like
protein/acidic protein precursor"
/protein_id="AAA80496.1"
/db_xref="GI:924624"
/translation="MARSLFPMALFVLAAMLFVAYEVAOOLCKAPSTPGLCFMDS
SKRKYCKERTGCHSKLQKCKLCTKRCVDFDKSSVKATLGEBAKLSEVLEERT
WME"
sig_peptide 57..134
mat_peptide 135..275
mat 276..371
/product="gamma-thionin-like protein"
mat_peptide 375..596
/product="acidic protein"
3'UTR 204 a 82 c 107 g 203 t
BASE COUNT
ORIGIN
Alignment Scores:

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Pred. No.: 5,84e-14 Length: 596
Score: 182.50 Matches: 41
Percent Similarity: 62.35% Conservative: 12
Best Local Similarity: 48.24% Mismatches: 29
Query Match: 41.01% Indels: 3
Gaps: 3
US-09-854-562-2 (1-83) x SU020591 (1-596)

Qy 1 MetAlaArgSerIleTyrrPheMetAlaPheLeuValLeuAla---ThrLeuPheValAla 19
Db 57 ATGGCTGCTTCATTCATTTCTTCATGCAATTTTGTCTGGCAATGATGCTTTGTTACC 116
Qy 20 TyrglyValGlnGlyLysGlnIleCys---CysLysGlnLeuThrLysProValLysCys 38
Db 117 TATAGGTAGAGCTCGCAAAATTTGGCAAGCACCAGCCAACTTCCCGAGATTATGT 176
Qy 39 SerSerAspProLeuCysGlnLysLeuCysMetGluLysGlnLysTyrglyLysPglYHis 58
Db 177 TTTATGACTCATCATCATAGAAAATATTGTATC--AAAGGAAATTTACTGCGTGACAT 233
Qy 59 CysPheThrIleLeuSerLysCysLeuCysMetLysArgCysAsnAlaIysThrLeuAla 78
Db 234 TGTAGCAAACTCCAAAGAGTGTCATGCACTAAGCCATGTTATTTGACAAATCTCA 293
Qy 79 ThrGluLeuLeuAla 83
Db 294 AGTGAAGTTAAAGCA 308

RESULT 8
LOCUS AB005250 549 bp mRNA linear PLN 19-JUN-1999
DEFINITION Nicotiana paniculata mRNA for gamma-thionin, complete cds.
ACCESSION AB005250
VERSION AB005250.1 GI:2251080
KEYWORDS gamma-thionin.
SOURCE Nicotiana paniculata
ORGANISM Nicotiana paniculata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
1 (sites)
Komori,T., Yamada,S. and Imaseki,H.
A cDNA clone for gamma-thionin from Nicotiana paniculata (Accession
No. AB005250) (F6R97-132)
Plant Physiol. 115, 314 (1997)
JOURNAL 2 (bases 1 to 549)
AUTHORS Komori,T.
TITLE Direct Submission
SUBMITTED (26-JUN-1997) Toshiyuki Komori, Plant Breeding and
Genetics Research Laboratory, Japan Tobacco Inc., 700 Higashibara,
Iwata, Shizuoka 438, Japan
(E-mail:Toshiyuki.Komori@pbgrl.jti.co.jp, Tel.0538-32-7116,
Fax:0538-32-8700)
FEATURES
Source
1..549
/organism="Nicotiana paniculata"
/mol_type="mRNA"
/db_xref="taxon:62141"
1..549
/gene="NpThiol"
48..368
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/product="gamma-thionin"
/protein_id="BAA21325.1"
/db_xref="GI:2251081"
/translation="MARSLCFMFAVLAAMLFVAYEVOASTCKASNTPGLCTTPK
PCRKACSEKRTDCKSKILRRCTCYRCPVFDGMITDGAENLAEBEETLAALLES
MMDN"
BASE COUNT 166 a 87 c 112 g 184 t
ORIGIN

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Percent Similarity: 51.14% Conservative: 9
 Best Local Similarity: 40.91% Mismatches: 28
 Query Match: 29.33% Indels: 15
 DB: 8 Gaps: 6

US-09-854-562-2 (1-83) x AF507975 (1-456)

QY 1 MetAlaArgSerIleTyrPheMetAlaPheLeuValIleuAla---ThrIeuPheValAla 19
 DB 68 ATGGCTGCTGCACATCTGTTCTTGGCGGTGCTACTGACATGATGATGATGCTTTGCTGCC 127
 QY 20 TyrGlyValGlnGlyLysGluIleCysCysLysGluLeuThrLysProValLysCysSer 39
 DB 128 TATGACCGCAGAGG-----GCACTTGCAAG-----GCGATGCGCA 166
 QY 40 Ser--AspProLeuCysGlnLys-----LeuCysMetGluLysGlnLys 53
 DB 167 ACATGGGATTCGCTGTATCAATATAAACCATGTATGCGCTGTGCAAAAAGGCAAG 226
 QY 54 TyrGlnAspGlyHisCysPheThrIleLeuSerLysCysLeuCysMetLysArgCys--- 72
 DB 227 TTCTCTATGAGGCTCCTCAGCAAAATACTCAGAGATGTCTGTCACTAAGAGGTGTGA 286
 QY 73 AsnAlaLysThrIeuAlaThrGlu 80
 DB 287 TTCGAAAAAACTGAGGCACTCA 310

RESULT 11

AF507976 602 bp mRNA linear PLN 19-MAR-2003
 LOCUS Petunia x hybrida floral defensin-like protein 2 (D2) mRNA,
 DEFINITION complete cds.

ACCESSION AF507976 GI:24817409

VERSION AF507976.1 GI:24817409
 KEYWORDS
 SOURCE
 ORGANISM

Petunia x hybrida
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; lamids; Solanales; Solanaceae; Petunia.

REFERENCE
 AUTHORS Lay,F.T., Brugliera,F. and Anderson,M.A.
 TITLE Isolation and Properties of Floral Defensins from Ornamental
 Tobacco and Petunia

JOURNAL Plant Physiol. 131 (3), 1283-1293 (2003)
 PUBMED 1264678

REFERENCE
 AUTHORS (bases 1 to 602)
 TITLE Direct Submission
 JOURNAL Submitted (30-APR-2002) Florigene Ltd, 16 Gippe St., Collingwood,
 Melbourne, Victoria 3066, Australia

FEATURES
 source
 1. 502
 /organism="Petunia x hybrida"
 /mol_type="mRNA"
 /cultivar="Old Glory Blue"
 /db_xref="taxon:4102"

gene

1. 602
 /gene="D2"
 /note="pD2"
 67. 372
 /gene="D2"
 /codon_start=1
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 /protein_id="AA064751.1"
 /db_xref="GI:24817410"
 /translation="MARSIQCPFAVAIIAMFAAYENBAGTCKAECPTWEGICINKAP
 CVKCKQPERFTGHCSTKILRCLCPKATEBATATLANEVVTMAEALVEEDMME"

CDS

BASE COUNT 221 a 102 c 114 g 165 t
 ORIGIN

Alignment Scores:
 Pred. No.: 3.97e-07

Length: 602

Score: 129.00 Matches: 35
 Percent Similarity: 50.57% Conservative: 9
 Best Local Similarity: 40.23% Mismatches: 37
 Query Match: 28.99% Indels: 6
 DB: 8 Gaps: 3

US-09-854-562-2 (1-83) x AF507976 (1-602)

QY 1 MetAlaArgSerIleTyrPheMetAlaPheLeuValIleuAla---ThrIeuPheValAla 19
 DB 67 ATGGCTGCTGCACATCTGTTCTTGGCGGTGCTACTGACATGATGATGATGCTTTGCTGCC 126
 QY 20 TyrGlyValGlnGlyLysGluIleCysCysLysGluLeuThrLysProValLysCysSer 39
 DB 127 TATGACCGCAGAGGAACTTGCAGAGCTGAATGCCAATCTGGAGAGAAATATGATC 186
 QY 40 SerAspProLeuCysGlnLysLeuCys--MetGluLysGluLysTyrGlnAspGlyHis 58
 DB 187 AATMAAGCCCATGTGTAAATGTGTGCAAGACACAAACCAAAAATTCACCGAGCGCAC 246
 QY 59 CysPheThrIleLeuSerLysCysLeuCysMetLysArgCysAsnAlaLys----- 75
 DB 247 TGCAGTAAATACTCCGAAAGATGCTATGCACTAAGCGGTGTCACTGAAGAGCAACT 306
 QY 76 ---ThrIeuAlaThrGluLeu 81
 DB 307 GCAACTTGGCTAAGAGGTA 327

RESULT 12

ST322R 470 bp mRNA linear PLN 09-MAY-1995
 LOCUS Potato mRNA for tuber protein (p322), put. proteinase inhibitor.
 DEFINITION X13180 M22140
 ACCESSION X13180.1 GI:21393

VERSION X13180.1 GI:21393
 KEYWORDS proteinase inhibitor; tuber protein.
 SOURCE Solanum tuberosum (potato)
 ORGANISM

Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; lamids; Solanales; Solanaceae; Solanum.

REFERENCE
 AUTHORS Stekema,W.J., Heidekamp,F., Dirkse,W.G., van Beekun,J., Haan,P.,
 ten Bosch,C. and Louwerse,J.D.
 TITLE Molecular cloning and analysis of four potato tuber mRNAs
 JOURNAL Plant Mol. Biol. 11, 255-269 (1988)

COMMENT p322 mature product AA seq shows 308 homology to that of soybean
 Bowman-Birk proteinase inhibitor

Data kindly reviewed (21-Jul-1989) by Stekema W.J.

FEATURES
 source
 1. 470
 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /cultivar="Bintje"
 /db_xref="taxon:4113"
 /clone="p322."
 /clone_1lb="pBR322"

CDS

7. 231
 /note="put. preprotein (AA -27 to 47)"
 /codon_start=1
 /protein_id="CA01577.1"
 /db_xref="GI:21394"
 /db_xref="SWISS-PROT:P03346"
 /translation="MRFAFAPFLIAMLVATKQPMIAEARHGESLSHRFGCTRD
 SNCAVCETERFSQGNCHGFRRCFTKPC"

sig_peptide

88. 228
 /product="putative mature protease inhibitor"

mat_peptide

231. 242
 /note="inverted repeat A"

repeat_unit

244. 255
 /note="inverted repeat A"

polyA_site

470

BASE COUNT 126 a 70 c 100 g 174 t /note="polYA site"

ORIGIN

Alignment Scores:

	Pred. No.:	Score:	Length:
	94.50	Matches: 23	470
	Percent Similarity: 46.58%	Conservative: 11	-
	Best Local Similarity: 31.51%	Mismatches: 32	-
Query Match:	21.24%	Indels: 7	-
DB:	8	Gaps: 3	-

US-09-854-S562-2 (1-83) x STJ32R (1-470)

Oy 6 TyrPheMetAlaPheLeuValLeuAlaThrLeuPheValAlaIleTyrGlyValcInglLys 25
:::|||||:::|||||:::
Db 13 TTCCTTGCTACTCTTTCTTCTTACTACTGTTCGGCGGCACCAAGATGGACCATTG 72
Oy 26 GluIleCys-----CylsYsgLueThrLysProValLys----CysSer 39
|||:::|||||:::|||||:::
Db 73 AGAATTGGAGAAGCAAGACCATTCGACGCGTTGACCATCTGTTCAAGAGCACCATGTAC 132
Oy 40 SerAspProLeuCysGlnLysLeucCysMetGluLysGluLysTyrGluAspGlyHisCys 59
133 AGAGTAGACCATTTGGCTTCCTGGATCGT---GAGACCGAAAGATTTCGGCGGCACATTGC 189
Oy 60 PheThrIleLeuSerLysCysLeucCysMetLysArgCys 72
190 CATGATTCCGTCGCCGCTTGTTCCTTGGACATAAGCATG 228
Db

RESULT 13

AP003272 139934 bp DNA linear PLN 29-MAR-2003

LOCUS AP003272

DEFINITION Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,

ACCESSION PAC clone:P0506E04.

VERSION AP003272 BA000010

KEYWORDS AP003272.3 GI:15623865

SOURCE ORGANISM

ORIGIN

REFERENCE

AUTHORS

1 Saseki,T., Matsumoto,T., Yamamoto,K., Sakata,K., Baba,T.,
Kataoyose,Y., Wu,J., Nilmuraz,Y., Cheng,Z., Nagamura,Y.,
Anteono,B.A., Kanamori,H., Hosoikawa,S., Masukawa,M., Arikawa,K.,
Chiden,Y., Hayashi,M., Okamoto,M., Ando,T., Aoki,H., Arita,K.,
Hamada,M., Harada,C., Hijishita,S., Honda M., Ichikawa,Y.,
Idonuma,A., Iijima,M., Ikeda,M., Ikemo,M., Itoh,S., Itoh,T.,
Itch,Y., Itch,Y., Iwabuchi,A., Kamiya,K., Karsawa,W., Katagiri,S.,
Kikuta,A., Kodayashi,N., Kono,I., Machida,K., Maehara,T.,
Mizuno,H., Mizubayashi,T., Mukai,Y., Nagasaki,H., Nakashima,M.,
Nakama,Y., Nakabayashi,Y., Nakamura,M., Namiki,N., Negishi,M.,
Oheta,I., Ono,N., Saiji,S., Sakai,K., Shibata,M., Shimokawa,T.,
Shomura,A., Song,J., Takasaki,Y., Terasawa,K., Tsuji,K., Waki,K.,
Yanagata,H., Yamane,H., Yoshiki,S., Yoshihara,R., Yukawa,K.,
Zhong,H., Iwama,H., Endo,T., Ito,H., Hahn,U.H., Kim,H.I., Eun,M.Y.,
Yano,M., Jiang,U. and Gojobori,T.
The genome sequence and structure of rice chromosome 1
Nature 420 (6913), 312-316 (2002)
2 (bases 1 to 139934)
Saseki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
Submitted (19-FEB-2001) Takui Saseki, National Institute of
Agrobiological Sciences, Rice Genome Research Program, Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:saseki@ibarc.affrc.go.jp URL:http://rsgp.dna.affrc.go.jp/
Tel:81-298-38-7441, Fax:81-298-38-7468)
On Sep 14, 2001 this sequence version replaced gi:15216345.
Genes were predicted from the integrated results of the following:

FEATURES
Source

GENSCAN. 0.0. BLASTN2.0, BLASTX2.0ae as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr (<http://ncbi.nlm.nih.gov/blast/cd>) and the cDNA sequence database at RGP. Protein homologs of the coding regions were searched against NCBI Nonredundant Protein database with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTN 2.0 with the corresponding DBD accession no. and RGP clone ID. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein. The orientation of the sequence is from S6 to T7 of the PAC clone. Annotated information on overlap and assembly quality together with annotation of this entry is available at <http://rgp.dna.affrc.go.jp/genomeSeq.html>.

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/db_xref="GI:15623869"

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/db_xref="GI:15623874"
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AIVGFVNGISKFDL"
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50892..51106,52016..52103,52216..52450)
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US-09-854-562-2 (1-83) x AP003272 (1-139934)

Alignment Scores:			
Pred. No.:	10.8	Length:	139934
Score:	90.50	Matches:	25
Percent Similarity:	51.56%	Conservative:	8
Best Local Similarity:	39.06%	Mismatches:	22
Query Match:	20.34%	Indels:	9
DB:	8	Gaps:	5

Oy -09-854-562-2 (1-83) x AP003272 (1-139934)

Oy 17 PheVALALATyrGlyValGLn-----GlyLysglu---IleCysCysLysGlu 31
Db 126487 TTTGTATTCTTACTCGTGATCATGATTTTACAGGCACAGAACTGATCATCTGCCAAGCA 126548

Oy 32 LeuThrLysProVal-----LysCysSerSerAspProLeuCysGlnLysLeuCysMet 49
Db 126547 AGAGCAAAATATACC GGCGGAAGTCAGGGGCAAGAAGCTGGCATGATCTGGTC 126606

Oy 50 GlnLysGlnLysTyrGlnAspGlyHisCysPheThr--IleLeuSerLysCysLeuCys 68
Db 126607 CAC---GAGGAGTACACCGCGGCTACTCTCCAAAGCGCGCTTCTCCAAGTGCATGTGC 126663

Oy 69 MetLysArgCys 72
Db 126664 ACCAACCGGTGT 126775

RESULT 14
AP003246

LOCUS AP003246 178649 bp DNA linear PLN 29-MAR-2003

DEFINITION Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,
PAC clone:P0423A12.

ACCESSION AP003246 BA000010

VERSION AP003246.3 GI:21104640

KEYWORDS

SOURCE ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pharbitidaceae; Oryzaceae; Oryza.

REFERENCE

AUTHORS Sasaki,T., Matsumoto,T., Yamamoto,K., Sakata,K., Baba,T.,
Kato,Yose,Y., Wu,O., Nilmura,Y., Cheng,Z., Nagamura,Y.,
Antonio,B.A., Kanamori,H., Hosokawa,S., Masukawa,M., Arikawa,K.,
Chiden,Y., Hayashi,M., Okamoto,M., Ando,T., Aoki,H., Arita,K.,
Hamada,M., Harada,C., Hijiishi,T., Honda,M., Ichikawa,Y.,
Idonuma,A., Iijima,M., Ikeda,M., Ikeno,M., Itob,S., Itob,T.,
Itou,Y., Itoh,Y., Iwabuchi,A., Kamiya,K., Katsasawa,M., Katagiri,S.,
Nakano,H., Kobayashi,N., Kono,I., Machita,K., Maehara,T.,
Minzuho,H., Miyabayashi,T., Mukai,Y., Nagasaki,H., Nakashima,M.,
Nakana,Y., Nakamichi,Y., Nakamura,M., Namiki,N., Negishi,M.,
Ohia,I., Ono,N., Saij,S., Sakai,K., Shibata,M., Shimokawa,T.,
Shomura,A., Song,J., Takazaki,Y., Terasawa,K., Teuji,K., Waki,K.,
Yamagata,H., Yamane,H., Yoshiki,S., Yoshihara,R., Yokawa,K.,
Zhong,H., Iwama,H., Endo,T., Ito,H., Hanh,J.H., Kim,H.I., Eun,M.Y.,
Yano,M., Jiang,J. and Gojobori,T.
The genome sequence and structure of rice chromosome 1
Nature 420 (6913), 312-316 (2002)

TITLE JOURNAL MEDLINE PubMed
22337376
12447438

Submitted (13-DEC-2000) Yuegang Zhou, Chongqing Institute of Technology, Department of Bioengineering, Xingsheng Road, Yangjiaping, Chongqing, Chongqing 400050, China, PRC

Job time : 2059 secs
Search completed: August 23, 2003, 07:40:18

Search completed: August 23, 2003, 07:46:18
Job time : 2059 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 23, 2003, 05:57:28 ; Search time 214 Seconds

(without alignments)
1046.978 Million cell updates/sec

Title: US-09-854-562-2

Perfect score: 445

Sequence: 1 MARSIFMAFLVLTFLVAV.....SKLCMKRCAKTLATLLELA 83

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Searched: 2552756 segs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	434.5	97.6	506	22 AAF83987	Pepper defensin pr
2	431.5	97.0	548	24 ABX12800	DNA encoding Capsi
3	189.5	42.6	566	20 AAV70142	Nicotiana excelsio
4	182.5	41.0	564	12 AAQ10262	Ovary tissue trans
5	182.5	41.0	564	14 AAQ34940	p2130 coding seque
6	182.5	41.0	564	17 AAT18823	Tomato p2130 cDNA
7	182.5	41.0	564	18 AAT48813	cDNA clone p2130 c
8	182.5	41.0	564	24 ABZ21970	Plasmid p2130 cDNA
9	177.5	39.9	558	20 AAV70143	Nicotiana panicula
10	156	35.1	456	20 AAV70141	Nicotiana excelsio
11	132	29.7	3528	17 AAT18824	Tomato p2130 genom
12	132	29.7	3528	18 AAT48816	Calgene lambda 140
13	132	29.7	3528	24 ABZ21971	Plasmid p2130 cDNA
14	132	29.7	4383	12 AAQ10263	p2130 contg. Calge
15	132	29.7	4383	12 AAQ10319	Calgene lambda 140
16	132	29.7	4383	14 AAQ35143	Calgene lambda 140
17	132	29.7	4383	14 AAQ34941	Calgene lambda 140
18	86.5	19.4	272	25 ABX28732	Human GDP-mannose
19	86.5	19.4	277	25 ABX29735	Human GDP-mannose
20	86.5	19.4	361	25 ABX19080	Human GDP-mannose
21	84.5	19.0	465	21 AAC34026	Arabidopsis thalia
22	84.5	19.0	520	21 AAC35542	Arabidopsis thalia
23	84	18.9	594	17 AAT16870	Pepper Group 2 pro
24	84	18.9	594	22 AAD18213	Pepper Group 2 pro
25	83.5	18.8	275	25 AAD18213	Human GDP-mannose
26	81	18.2	234	24 ABZ12813	Arabidopsis thalia
27	81	18.2	425	25 ABX62145	Arabidopsis thalia
28	79	17.8	225	22 AAF83988	Pepper thionin-lik
29	79	17.8	2000	24 ABZ15483	Arabidopsis thalia
30	77.5	17.4	597	24 AAC40605	Arabidopsis thalia
31	77	17.3	294	24 ABX12237	Corn tassels derive
32	76.5	17.2	2297	22 AAZ29909	C albicans apoptos
33	74.5	16.7	1216	21 AAZ24468	Mouse 15 Kda selen
34	74	16.6	403	19 AAV10632	A. thaliana PDF1.1
35	74	16.6	697	21 AAF14323	Aspergillus oryzae
36	73.5	16.5	2263	21 AAC76109	Human ORFX ORF1664
37	73.5	16.5	2410	22 AAK94348	Human full-length
38	73.5	16.5	2569	24 ABN93360	Human secreted pro
39	73.5	16.5	5593	22 AAF83879	Human cDNA encodin
40	73.5	16.5	5586	22 AAF83878	Tumour suppressor
41	73.5	16.5	5586	24 ABL34183	Human immune syste
42	73.5	16.5	9182	23 ABL04532	Drosophila melanog
43	73	16.4	282	21 AAC65603	Arabidopsis thalia
44	73	16.4	334	21 AAC35620	Arabidopsis thalia
45	72.5	16.3	264	25 ABX31561	Human GDP-mannose

ALIGNMENTS

RESULT 1	
AAAF83987	standard; cDNA to mRNA, 506 BP.
AAAF83987	
AAAF83987	
22-AUG-2001	(first entry)
Pepper defensin protein gene, PeppDef cDNA sequence.	
Pepper defensin, PeppDef; thionin-like protein, PeppTh; transgenic;	
phytopathogen; antimicrobial; ss.	
Capsicum annuum.	
Key	Location/Qualifiers
CDS	10..264

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FT      /*tag= a
FT      /product= "defensin protein"
FT      /gene= "Pepdef"
PN      EPI101771-AL.
PD      23-MAY-2001.
XX      15-NOV-1999; 99EP-0309059.
XX      15-NOV-1999; 99EP-0309059.
PR      (KOU-) KOREA KUMHO PETROCHEMICAL CO LTD.
PA      Oh B, Ko MK, Shin B, Chung CH;
PI      WPI; 2001-357927/38.
DR      P-Psdb; AAB85079.
XX      New pathogen induced genes (pepper defensin protein gene and pepper
XX      thionin-like protein gene) from Capsicum annuum, useful for producing
XX      transgenic plants with enhanced resistance against phytopathogens, e.g.
XX      fungi or nematode
XX      Claim 3; Page 10-11; 22pp; English.
XX      The invention provides new isolated nucleic acid molecules encoding a
XX      pepper defensin protein (Pepdef) and a pepper thionin-like protein
XX      (Pepthi). The Pepdef and Pepthi genes are useful for producing transgenic
XX      plants that exhibit enhanced resistance against phytopathogens, e.g.
XX      fungi, bacteria, viruses, nematode, mycoplasma-like organisms, parasitic
XX      higher plants, flagellate protozoa or insects. The present sequence
XX      represents the cDNA sequence of the Pepdef gene.
SQ      Sequence 506 BP; 174 A; 74 C; 96 G; 162 T; 0 other;

Alignment Scores:
Pred. No.: 7,43e-45 Length: 506
Score: 434.50 Matches: 83
Percent Similarity: 98.81% Conservative: 0
Best Local Similarity: 98.81% Mismatches: 0
Query Match: 97.64% Indels: 1
DB: 22 Gaps: 1

US-09-854-562-2 (1-83) x AAF83987 (1-506)
OY      1 MetAlaArgSerIleTyrPheMetAlaPheLeuValIleuAla---ThrlaupheValAla 19
DB      10 ATGGCTCGTTCATTACTTTCATGCGATTCTTGCTTGGCAATGACACTCTTTGTTGCT 69
OY      20 TyrgIyValGInglYLySGIuileCySGIySGIuLeuThrlYsProValIySGySer 39
DB      70 TATGGGGGTGCAAGCAAGCAAGCAATTTGCTGTAAAGGCTCACAAACTGTTAAATGTTCT 129
OY      40 SerAaPProLeuCySGIuLyLeuCySGMetGluLySGIuLySTyrgIuAaPGLyHicGyS 59
DB      130 AATGACCCCTCTATGTCAAAACCTCTGTATGAGAGAGAAATATGAAGATGCTCATTTGT 189
OY      60 PheThrlleuSerIySGIySGIuLeuCySGMetIySAySGyASaAlaIySThrlleuAlaThr 79
DB      190 TTCACAACTCTTAAGCAAGTGTATGATGAAGAATGTAAATGCTAAACTCTGCCAACA 249
OY      80 GIuLeuLeuAla 83
DB      250 GAATTGCTTGTCT 261

RESULT 2
ID      ABX12800 standard; DNA; 548 BP.
XX      ABX12800;
XX      29-MAY-2003 (first entry)

```

```

XX      DNA encoding Capsicum annuum L. cv. Hanbyul thionine.
DE      Thionine; plant disease resistance; plant; gene; ds.
XX      Capsicum annuum L. cv. Hanbyul.
XX      Capsicum annuum L. cv. Hanbyul.
XX      Key
XX      CDS
XX      Location/Qualifiers
XX      FT
XX      CDS
XX      52..306
XX      /*tag= a
XX      /product= "Thionine"
XX      /trans_except= (pos:64..66,aa:Thr)
XX      /trans_except= (pos:271..273,aa:Xaa)
XX      /note= "Xaa is given as "Net" in the specification"
XX      KR2002024732-A.
XX      PD
XX      01-APR-2002.
XX      26-SEP-2000; 2000KR-0056518.
XX      26-SEP-2000; 2000KR-0056518.
XX      (KOC-) KOREA CHUNGANG EDUCATIONAL FOUND.
XX      Hwang BG, Kim YJ, Lee SC;
XX      WPI; 2002-747901/81.
XX      P-Psdb; ABU08325.
XX      Thionine gene of capsicum annuum L. cv. hanbyul and probing method of
XX      resistance for plant diseases -
XX      Example 1; Fig 1; 14pp; Korean.
XX      The present invention relates to the thionine gene of Capsicum
XX      annuum L. cv. Hanbyul, and a probing method of resistance for
XX      plant diseases, caused by Xanthomonas campestris subsp. vesicatoria,
XX      Collectotrichum coccodes, Collectotrichum gloeosporioides and the like.
XX      The presents sequence encodes capsicum annuum L. cv. Hanbyul thionine.
SQ      Sequence 548 BP; 188 A; 76 C; 105 G; 179 T; 0 other;

Alignment Scores:
Pred. No.: 1.95e-44 Length: 548
Score: 431.50 Matches: 82
Percent Similarity: 98.81% Conservative: 1
Best Local Similarity: 97.62% Mismatches: 0
Query Match: 96.97% Indels: 1
DB: 24 Gaps: 1

US-09-854-562-2 (1-83) x ABX12800 (1-548)
OY      1 MetAlaArgSerIleTyrPheMetAlaPheLeuValIleuAla---ThrlaupheValAla 19
DB      52 ATGGCTCGTTCATTACTTTCATGCGATTCTTGCTTGGCAAGCAAGCTTTGTTGCT 111
OY      20 TyrgIyValGInglYLySGIuileCySGIySGIuLeuThrlYsProValIySGySer 39
DB      112 TATGGGGGTGCAAGCAAGCAAGCAATTTGCTGTAAAGGCTCACAAACTGTTAAATGTTCT 171
OY      40 SerAaPProLeuCySGIuLyLeuCySGMetGluLySGIuLySTyrgIuAaPGLyHicGyS 59
DB      172 AATGACCCCTCTATGTCAAAACCTCTGTATGAGAGAGAAATGTGAAGATGCTCATTTGT 231
OY      60 PheThrlleuSerIySGIySGIuLeuCySGMetIySAySGyASaAlaIySThrlleuAlaThr 79
DB      232 TTCACAACTCTTAAGCAAGTGTATGATGAAGAATGTAAATGCTAAACTCTGCCAACA 291
OY      80 GIuLeuLeuAla 83
DB      292 GAATTGCTTGTCT 303

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RESULT 3

Db 270 AAAACAGAGCTGAACTTAGCTGAGAA 299

RESULT 4

Db . |||. |||:: :||| |
100 TATGAGCTAGACGTGCGCAATTTCGAAGCACCACCAACTTTCCACAGATTATGT 15

QY 39 SerSerAppProLeuCyGlnLysLeuCyMetGluLysGlyGluAspGlyHis 58
 DB 160 TTTATGACATCATGTAGAAAATATTGTATC--AAAGGAAATTTACTGGTGACAT 216
 QY 59 CysPheThrIleLeuSerLysCysLeuCyMetLysArgCysAsnAlaLysThrLeuAla 78
 DB 217 TGTAGCAAACTCCAAAGGAAGTGTCTATGCACTAAGCAGATGTATTGACAAATCTCA 276
 QY 79 ThrGluLeuLeuAla 83
 DB 277 AGTGAAGTTAAAGCA 291
 RESULT 5
 AA034940
 ID AA034940 standard; DNA; 564 BP.
 AC AA034940;
 XX
 DT 25-MAR-2003 (updated)
 DT 19-MAY-1993 (first entry)
 XX
 DE p2130 coding sequence.
 XX
 KW cDNA; clone p2130; antisense; tomato; ovary; integument; outer pericarp;
 KW fruit; development; transcription; initiation; region; modulation;
 KW ovary-specific; endogenous; fruit product; exogenous; phenotype; ds.
 XX
 OS Lycopersicon esculentum.
 XX
 FH Key Location/Qualifiers
 FT misc_RNA 447..564
 FT /*tag= a
 FT /note= "Corresponds to p27 cDNA"
 XX
 PN US5175095-A.
 PD 29-DEC-1992.
 XX
 PF 17-JUL-1990; 90US-0554195.
 XX
 PR 19-JUL-1989; 89US-0382518.
 PR 17-JUL-1990; 90US-0554195.
 XX
 PA (CALJ) CALGENE INC.
 XX
 PI Houck CM, Martineau BW;
 XX
 DR WPI; 1993-026940/03.
 DR P-PSDB; AAR30779.
 PT DNA constructs contg. tomato p2130 transcriptional initiation
 PT region - useful for modulation of endogenous fruit prods. and for
 PT prodn. of exogenous prods.
 XX
 PS Disclosure: Fig 1; 18pp; English.
 XX
 CC The sequence given shows the DNA sequence of cDNA clone p2130. This
 CC sequence is expressed during the early stages of anthesis in tomatoes.
 CC The message is expressed in ovary integument and ovary outer pericarp
 CC tissue. It is not readily detectable in other tissues or at other
 CC stages of fruit development. The transcription initiation region
 CC associated with this gene is therefore considered to be ovary-
 CC specific. The actual function of the p2130 polypeptide is unknown.
 CC The transcription initiation region can be used for modulation of
 CC endogenous fruit products, for production of exogenous products and
 CC for modification of the phenotype of fruit and fruit products.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 PS Sequence 564 BP; 188 A; 80 C; 107 G; 189 T; 0 other;
 SQ
 Alignment Scores: 1.96e-13 Length: 564
 Pred. No.:

Score: 182.50 Matches: 41
 Percent Similarity: 62.35% Conservative: 12
 Best Local Similarity: 48.24% Mismatches: 29
 Query Match: 41.01% Indels: 3
 DB: 14 Gaps: 3
 US-09-854-562-2 (1-83) x AA034940 (1-564)
 QY 1 MetAlaArgSerIleTyPheMetAlaPheLeuValLeuAla---ThrLeuPheValAla 19
 DB 40 ATGGCTGTTCCATTTCTTCATGCGCATTTTGGTCTGGCAATGATGCTCTTTGTTACC 99
 QY 20 TyrGlyValGlnGlyLysGluLysCys---CysLysGluLeuThrLysProValLysCys 38
 DB 100 TATAGGTAGAGAGCTCCAGAAATTTGCCAAGCACCAAGCCAACTTCCAGAGATTATGT 159
 QY 39 SerSerAppProLeuCyGlnLysLeuCyMetGluLysGlyGluAspGlyHis 58
 DB 160 TTTATGACATCATGTAGAAAATATTGTATC--AAAGGAAATTTACTGGTGACAT 216
 QY 59 CysPheThrIleLeuSerLysCysLeuCyMetLysArgCysAsnAlaLysThrLeuAla 78
 DB 217 TGTAGCAAACTCCAAAGGAAGTGTCTATGCACTAAGCAGATGTATTGACAAATCTCA 276
 QY 79 ThrGluLeuLeuAla 83
 DB 277 AGTGAAGTTAAAGCA 291
 RESULT 6
 AAT31823
 ID AAT31823 standard; cDNA; 564 BP.
 AC AAT31823;
 XX
 DT 25-MAR-2003 (updated)
 DT 14-SEP-1996 (first entry)
 XX
 DE Tomato p2130 cDNA clone.
 XX
 KW Ovary; ovule; fruit; tomato; cotton; melanin; vector;
 KW transgenic plant; ss.
 XX
 OS Lycopersicon esculentum cv. UC82B.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..357
 FT /*tag= a
 XX
 PN US5530185-A.
 PD 25-JUN-1996.
 XX
 PF 29-DEC-1992; 92US-0998158.
 XX
 PR 29-DEC-1992; 92US-0998158.
 PR 19-JUL-1989; 89US-0382518.
 PR 17-JUL-1990; 90US-0554195.
 XX
 PA (CALJ) CALGENE INC.
 XX
 PI Martineau BW, Reilley AA, Stalker DW;
 XX
 DR WPI; 1996-308822/31.
 DR P-PSDB; AAR97559.
 PT DNA construct for expressing melanin synthesis gene in plant ovule
 PT cells - contains promoter from the tomato p2130 gene, also binary
 PT vector and transgenic plants, esp. cotton, contg. construct
 XX
 PS Example 3; Fig 1A-B; 25pp; English.
 XX
 CC The tomato p2130 clone contains a 564 bp insert of cDNA (AAT31823)
 CC detected only in a tomato cDNA library prepd. from pre-anthesis

CC RNA. It was isolated by screening a library prep. from cDNA
 CC of pre-anthesis stage ovaries with probes made from pre-anthesis
 CC mRNA, leaf mRNA and young seedling mRNA. The insert was used to
 CC isolate the corresponding genomic clone (AAT31824). The p2130
 CC transcriptional initiation region is considered to be ovary-specific.
 CC It can be utilised in DNA constructs for the expression of
 CC heterologous genes, partic. in early fruit development, and esp. for
 CC expression of a melanin synthesis gene in transgenic cotton. The
 CC native function of the p2130 gene product (AAR7559) is unknown.
 CC (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 564 BP; 188 A; 80 C; 107 G; 189 T; 0 other;

Alignment Scores:

Pred. No.:	1.96e-13	Length:	564
Score:	182.50	Matches:	41
Percent Similarity:	62.35%	Conservative:	12
Best Local Similarity:	48.24%	Mismatches:	29
Query Match:	41.01%	Indels:	3
DB:	17	Gaps:	3

US-09-854-562-2 (1-83) x AAT31823 (1-564)

Oy 1 MetAlaArgSerIleTyRPhemeAlaPheLeuValLeuA1a---ThrLeuPheValA1a 19
 Db 40 ATGGCTGCTTCATTTCTTCATGCAATTTTGGCTTGGCAATGATGCTCTTTGTTACC 99
 Oy 20 TyrclyValGinglyLysGluIleCys---CysLysGluLeuThrLysProValIleCys 38
 Db 100 TATAGGAGTGAAGCTCCAAAGCAATTTGGCAAGCACCACCAACTTCCCGAGATTATGT 159
 Oy 39 SerSerAspProLeuCysGlnLysLeuCysMetGluLysGluLysTyrclyLysGluAspGlyHis 58
 Db 160 TTTATGAGCTCATCATGTAAGAAATATGTATC---AAAGGAATTTACTGCTGGACAT 216
 Oy 59 CysPheThrIleLeuSerLysCysLeuCysMetLysArgCysAsnAlaLysThrLeuA1a 78
 Db 217 TGTAGCAAACTCCAAAGAGAGTGTATGCACTAAGCATGTGATTTGACAAATCTCA 276

Oy 79 ThrGluLeuLeuA1a 83

Db 277 AGTGAAGTTAAAGCA 291

RESULT 7

AAT48813
 ID AAT48813 standard; cDNA; 564 BP.

XX AC AAT48813;

XX DT 14-MAR-1997 (first entry)

XX DE cDNA clone p2130 capable of directing ovary-tissue transcription.

XX KM Ovary; fruit; colour; pigmentation; cotton; tomato; probe;

XX KM promoter; p2130; p27; transgenic plant; ds.

XX OS Lycopersicon esculentum cv. UC82B.

XX FH Key Location/Qualifiers

FT CDS 1..357

FT misc_RNA 447..564

FT /tag= a

FT /note= "bases 447-564 correspond to clone p27"

XX MO9640951-A2.

XX PD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US09911.

XX PR 07-JUN-1995; 95US-0487087.

PA (CALJ) CALGENE INC.

XX McBride K, Stalker DM;

XX WPI; 1997-052341/05.

DR P-PSDB; AAW08364.

XX DNA construct capable of directing ovary-tissue transcription in

PT plants - useful for modifying colour phenotype, in e.g. cotton

PS Example 1; Fig 1; 75pp; English.

XX A cDNA clone (AAT48813), designated p2130, comprises a tomato
 CC transcriptional initiation region that is capable of directing
 CC tissue, partic. early in fruit development, e.g. to modify colour
 CC phenotype. It can also be used as a molecular probe. To obtain
 CC p2130, a tomato pre-anthesis stage cDNA library was screened by
 CC differential hybridisation. Clones p27 and p28 that hybridised
 CC only to pre-anthesis probes were used to screen a second cDNA
 CC library, yielding p2130 and p270 (see also AAT48814). A genomic
 CC clone (AAT48816) was also isolated using p2130 as probe.

XX SQ Sequence 564 BP; 188 A; 80 C; 107 G; 189 T; 0 other;

Alignment Scores:

Pred. No.:	1.96e-13	Length:	564
Score:	182.50	Matches:	41
Percent Similarity:	62.35%	Conservative:	12
Best Local Similarity:	48.24%	Mismatches:	29
Query Match:	41.01%	Indels:	3
DB:	18	Gaps:	3

US-09-854-562-2 (1-83) x AAT48813 (1-564)

Oy 1 MetAlaArgSerIleTyRPhemeAlaPheLeuValLeuA1a---ThrLeuPheValA1a 19
 Db 40 ATGGCTGCTTCATTTCTTCATGCAATTTTGGCTTGGCAATGATGCTCTTTGTTACC 99
 Oy 20 TyrclyValGinglyLysGluIleCys---CysLysGluLeuThrLysProValIleCys 38
 Db 100 TATAGGAGTGAAGCTCCAAAGCAATTTGGCAAGCACCACCAACTTCCCGAGATTATGT 159
 Oy 39 SerSerAspProLeuCysGlnLysLeuCysMetGluLysGluLysTyrclyLysGluAspGlyHis 58
 Db 160 TTTATGAGCTCATCATGTAAGAAATATGTATC---AAAGGAATTTACTGCTGGACAT 216
 Oy 59 CysPheThrIleLeuSerLysCysLeuCysMetLysArgCysAsnAlaLysThrLeuA1a 78
 Db 217 TGTAGCAAACTCCAAAGAGAGTGTATGCACTAAGCATGTGATTTGACAAATCTCA 276

Oy 79 ThrGluLeuLeuA1a 83

Db 277 AGTGAAGTTAAAGCA 291

RESULT 8

ABZ21970
 ID ABZ21970 standard; cDNA; 564 BP.

XX AC ABZ21970;

XX DT 28-MAR-2003 (first entry)

XX DE Plasmid p2130 cDNA sequence p27.

XX KM Transcriptional factor; ovary tissue; gene; ss.

XX OS Unspecified.

XX FH Key Location/Qualifiers

FT CDS 1..564

FT /tag= a

FT /partial

```

FT      /product= "p2130 protein sequence"
FT      /trans_except= (pos:355..357,aa:Xaa)
FT      /trans_except= (pos:358..360,aa:Xaa)
FT      /trans_except= (pos:376..378,aa:Xaa)
FT      /trans_except= (pos:385..387,aa:Xaa)
FT      /trans_except= (pos:436..438,aa:Xaa)
FT      /trans_except= (pos:454..456,aa:Xaa)
FT      /trans_except= (pos:478..480,aa:Xaa)
FT      /trans_except= (pos:490..492,aa:Xaa)
FT      /trans_except= (pos:541..543,aa:Xaa)
FT      /note= "all Xaa's are encoded by stop codons"
XX
XX      CNI189856-A.
XX
XX      PD      05-AUG-1998.
XX
XX      PF      07-JUN-1996; 96CN-0195170.
XX
XX      PR      07-JUN-1995; 95US-0480087.
XX
XX      PA      (CALJ ) CALGENE INC.
XX
XX      DR      WPI; 2002-733392/80.
XX      DR      P-PSDB; ABB56255.
XX
XX      PT      Use of transcriptional factors of ovary tissue -
XX
XX      PS      Example 3; Fig 1A-B; 56pp; Chinese.
XX
XX      CC      The present invention describes the use of transcriptional factors of
XX      CC      ovary tissue. The present sequence represents a nucleotide sequence
XX      CC      which is used in an example from the present invention.
XX
XX      SQ      Sequence 564 BP; 188 A; 80 C; 107 G; 189 T; 0 other;
XX
Alignment Scores:
Pred. No.: 1,966-13 Length: 564
Score: 182.50 Matches: 41
Percent Similarity: 62.35% Conservative: 12
Best Local Similarity: 48.24% Mismatches: 29
Query Match: 41.01% Indels: 3
DB: 24 Gaps: 3
US-09-854-562-2 (1-83) x AB221970 (1-564)
OY      1 MetAlaArgSerIleTyrPheMetAlaPheLeuValLeuAla---ThrLeuPheValAla 19
DB      40 ATGGCTCGTTCATTTCTTCATGGCATTTTGGCTTGGCAATGATGCTTTGTTACC 99
OY      20 TyrGlyValGlnGlyLysGluIleCys---CysLysGluLeuThrLysProValLysCys 38
DB      100 TATAGGTGAGTGAAGCTCAGCAAAATTTGCAAGCAGCAAGCCAAACTTTCCAGGATTATGT 159
OY      39 SerSerAspProLeuCysGlnLysLeuCysMetGluLysGluLysTyrGluAspLysHis 58
DB      160 TTTATGACCTCATCTATGTAAGAAATATTGTATC---AAGAGCAATTTACTGGTGGACAT 216
OY      59 CysPheThrIleLeuSerLysCysLeuCysMetLysArgCysAsnAlaLysThrLeuAla 78
DB      217 TGTAGCAAAATCCCAAGAGAGTCTATGACACTAAGCATGTGATTTTGACAAATCTCA 276
OY      79 ThrGluLeuLeuAla 83
DB      277 AGTGAAGTTAAAGCA 291
XX
XX      RESULT 9
XX      ID      AAV70143 standard; cDNA to mRNA; 558 BP.
XX      AC      AAV70143;
XX      DT      03-FEB-1999 (first entry)

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```

DE      Nicotiana paniculata thionine gene NpTH1.
XX      Nicotiana excelsior; Nicotiana paniculata; thionine; NpTH1; NpTH12;
XX      NpTH1; salt stress; resistance; ds.
XX      Nicotiana paniculata.
XX      Nicotiana paniculata.
XX      Key      Location/Qualifiers
XX      CDS      48..368
XX      FT      /*tag= a
XX
XX      JPI0295380-A.
XX
XX      PD      10-NOV-1998.
XX
XX      PF      23-APR-1997; 97JP-0120179.
XX
XX      PR      23-APR-1997; 97JP-0120179.
XX
XX      PA      (NISR ) JAPAN TOBACCO INC.
XX
XX      DR      WPI; 1999-038278/04.
XX      DR      P-PSDB; AAM83133.
XX
XX      PT      Thionine gene derived by salt stress - used to deliver improved salt
XX      PT      stress to plants
XX
XX      PS      Claim 5; Page 5-6; 6pp; Japanese.
XX
XX      CC      The present sequence represents a thionine gene from Nicotiana
XX      CC      paniculata derived NpTH1. The thionine protein has an effect of
XX      CC      improving the salt stress resistance of a plant. The gene can improve
XX      CC      the salt stress resistance of a plant.
XX
XX      SQ      Sequence 558 BP; 175 A; 87 C; 112 G; 184 T; 0 other;
XX
Alignment Scores:
Pred. No.: 8,116-13 Length: 558
Score: 177.50 Matches: 45
Percent Similarity: 53.00% Conservative: 8
Best Local Similarity: 45.00% Mismatches: 28
Query Match: 39.89% Indels: 19
DB: 20 Gaps: 4
US-09-854-562-2 (1-83) x AAV70143 (1-558)
OY      1 MetAlaArgSerIleTyrPheMetAlaPheLeuValLeuAla---ThrLeuPheValAla 19
DB      48 ATGGCTCGTTCCTTCTGCTCATGGCATTTGCACTTTGGCAATGATGCTTTGTTGCC 107
OY      20 TyrGlyValGlnGlyLysGluIleCysCysLysGluLeu---ThrLysProValLysCys 38
DB      108 TATAGGTGAGTGAAGCTAAGTACTGTAAGCAAGCAAGCAATCATTTCCCTGGATTATGC 167
OY      39 SerSerAspProLeuCysGlnLysLeuCysMetGluLysGluLysTyrGluAspLysHis 58
DB      168 ATTACCAACCAACCATCCAGAAAAGCTTGTCTC---AGTGAAGAAATTTACTGATGAAAA 224
OY      59 CysPheThrIleLeuSerLysCysLeuCysMetLysArgCys----- 72
DB      225 TGTAGCAAAATCCCTCAAGAGTGTATTTGCTACAGCAAGCATGTGATTTGATGAAAGATG 284
OY      73 -----AsnAlaLysThrLeuAlaThrGluLeu 82
DB      285 ATCCAAACAGAGAGCTGAATAATTTGGCCGAGAGAGCAAGAAACTTTGGCTGAGCTTGTCTT 344
XX
XX      RESULT 10
XX      ID      AAV70141 standard; cDNA to mRNA; 456 BP.
XX      AC      AAV70141;
XX      DT      03-FEB-1999 (first entry)

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```

XX DE Nicotiana excelsior thionine gene NETH1.
XX KM Nicotiana excelsior; Nicotiana paniculata; thionine; NETH1; NETH12;
XX KW NETH1; salt stress; resistance; ds.
XX OS Nicotiana excelsior.
XX FT Key Location/Qualifiers
XX CDS 1..240
XX /*tag= a
XX PN JP10295380-A.
XX PD 10-NOV-1998.
XX PF 23-APR-1997; 97JP-0120179.
XX PR 23-APR-1997; 97JP-0120179.
XX PA (N1SB ) JAPAN TOBACCO INC.
XX DR WP1; 1999-038278/04.
XX P-PSDB; AAW83131.
XX PT Thionine gene derived by salt stress - used to deliver improved salt
XX stress to plants
XX PS Claim 1; Page 4; 6pp; Japanese.
XX CC The present sequence represents a thionine gene from Nicotiana excelsior
XX derived NETH1. The thionine protein has an effect of improving the salt
XX stress resistance of a plant. The gene can improve the salt stress
XX resistance of a plant.
XX SQ Sequence 456 BP; 149 A; 73 C; 88 G; 146 T; 0 other;

Alignment Scores:
Pred. NO.: 2.95e-10 Length: 456
Score: 156.00 Matches: 34
Percent Similarity: 68.18% Conservative: 11
Best Local Similarity: 51.52% Mismatches: 17
Query Match: 35.06% Indels: 4
DB: 20 Gaps: 4

US-09-854-562-2 (1-83) x AAV70141 (1-456)
QY 16 LeuPheValAlaIatYrGlyValGInGlyLeuGlyLeuGlyLeuThrIysPro 35
Db 1 CTCCTTGTGCTTATGAGTGCAGAGCTAGAGAAA---TCCGAGAGAGAAATTTTCACGGA 57
QY 36 ValIysCysSerSerAspProLeuGlyGlnIysLeuGlyGlnIysLeuGlyGln 55
Db 58 CTA---TGCATTACCAATCCACAAATGACAGAAAGCTGTATC---AAAGAGAAATTTACT 111
QY 56 AspGlyHisCysPheThrIleuSerIysCysLeuGlyGlnIysLeuGlyGlnIys 74
Db 112 GATGCTATTGTACCAAAATCTCGAAGAGGTCTATGACTAAGCCATGACAGAGACT 171
QY 75 LysThrLeuAlaThrGlu 80
Db 172 GAAACTTTAGCTGAGGA 189

RESULT 11
AA1824
ID AA1824 standard; cDNA; 3528 BP.
XX
XX AA1824;
XX
XX 25-MAR-2003 (updated)
XX 14-SEP-1996 (first entry)
XX
XX Tomato p2130 genomic clone Calgene Lambda 140.

```

```

XX XX Ovary; ovule; fruit; tomato; cotton; melanin; vector;
XX KM transgenic plant; ss.
XX OS Lycopersicon esculentum cv. UC82B.
XX FT Key Location/Qualifiers
XX CDS 586
XX misc_difference 586
XX /*tag= a
XX /note= "base n at position 586 is unidentified"
XX FT misc_difference 590
XX /*tag= b
XX /note= "base n at position 590 is not identified"
XX FT misc_difference 591
XX /*tag= c
XX /note= "base n at position 591 is not identified"
XX FT misc_difference 663
XX /*tag= d
XX /note= "base n at position 663 is not identified"
XX FT misc_difference 667
XX /*tag= e
XX /note= "base n at position 667 is not identified"
XX FT misc_difference 769
XX /*tag= f
XX /note= "base n at position 769 is not identified"
XX FT misc_difference 2483
XX /*tag= g
XX /note= "base 2483 is given as s in the
XX specification"
XX FT misc_difference 2485
XX /*tag= h
XX /note= "base 2485 is given as s in the
XX specification"
XX FT exon
XX /*tag= i
XX /note= 2567..2701
XX FT intron
XX /*tag= j
XX /note= 2702..2921
XX FT exon
XX /*tag= k
XX /note= 2922..3528
XX
XX US5530185-A.
XX 25-JUN-1996.
XX
XX 29-DEC-1992; 92US-0998158.
XX
XX 29-DEC-1992; 92US-0998158.
XX 19-JUL-1989; 89US-0382518.
XX 17-JUL-1990; 90US-0554195.
XX
XX (CALJ ) CALGENE INC.
XX Martineau BM, Reilley AA, Stalker DM;
XX WP1; 1996-30882/31.
XX P-PSDB; AAR97559.
XX
XX DNA construct for expressing melanin synthesis gene in plant ovule
XX cells - contains promoter from the tomato p2130 gene, also binary
XX vector and transgenic plants, esp. cotton, contg. construct
XX
XX Example 5; Fig 2A-C; 25pp; English.
XX
XX The tomato p2130 genomic clone (AA1824) was isolated from a genomic
XX library using a p2130 cDNA clone (AA1823) as probe. The p2130
XX transcriptional initiation region is considered to be ovary-specific.
XX It can be utilised in DNA constructs for the expression of
XX heterologous genes, partic. in early fruit development, and esp. for
XX expression of a melanin synthesis gene in transgenic cotton. The
XX native function of the p2130 gene product (AAR97559) is unknown.
XX (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 3528 BP; 1191 A; 529 C; 518 G; 1282 T; 8 other;
XX SQ

```

Alignment Scores:

Pred. No.:	4,21e-06	Length:	3528
Score:	132.00	Matches:	42
Percent Similarity:	33.33%	Conservative:	11
Best Local Similarity:	26.42%	Mismatches:	29
Query Match:	29.66%	Indels:	77
DB:	17	Gaps:	4

US-09-854-562-2 (1-83) x: AAT31824 (1-3528)

```

OY      1 MetAlaArgSerIleTyRheMeAlaPheLeuValIleuA1a---ThrLeuPheValA1a 19
DB      2638 ATGGCTGCTTCATTTCTTCATGCGCATTTTGGTCTGGCAATGATGCTCTTGTGTAC 2697
OY      20 TyrGlyValGlnGly-----
DB      2698 TATGCTTGTCTTCATTAATTTATTCCTAAATCATCGCATTAATAAATATGTAACG 2757
OY      25 LysGluIleCysCysLysGluLeuThrLys-ProValLys-----
DB      2758 AAGCAGACATCAGTAACCGTTTAATTAACCCCTAAATAATTGGAATGATATTACTT 2817
OY      37 -----
DB      2818 GCTATACGTTTAACAACATATGATAAAAAAACCTAAATAATATTCATTTGCTCT 2877
OY      37 -----
DB      2878 CTCATCATGTTATCTAATCTATTTTGTGTGATGATGTAAGAGTGAAGCTCAGCA 2937
OY      38 -----
DB      2938 AATTGCAAGACCAACCAAACTTCCAGATTATGTTTATGACATCATCATGTAG 2997
OY      45 nLysLeuCyMeGluLysGluLeuThyGluAspGlyHisCysPheThrIleLeuSerLy 65
DB      2998 AAAATATTGTATC---AAAGAGAAATTTACTGCTGAGACATGTGTAGCAAACTCCAAAGCA 3054
OY      65 sCysLeuCyMeGluLysGluLeuThyGluAspGlyHisCysPheThrIleLeuSerLy 83
DB      3055 GTGCTATGCACTTAAGCAGCATGTGTTATTTGACAAATCTCAAGTGAAGTTAAAGCA 3109

RESULT 12
AAT48816
ID AAT48816 standard; cDNA; 3528 BP.
XX AC
XX AAT48816;
XX
DT 14-MAR-1997 (first entry)
XX
DE Calgene Lambda 140 genomic clone.
XX
XX Ovary; fruit; colour; pigmentation: cotton; tomato; probe;
KM promoter; pZ130; pZ7; transgenic plant; ss.
XX
XX Lycopersicon esculentum cv. UC82B.
XX
XX Key Location/Qualifiers
FH exon /tag= a
FT exon 2567..2701
FT intron /tag= b
FT intron 2702..2921
FT exon /tag= c
FT exon 2922..3528
FT misc_RNA /tag= d
FT misc_RNA 2599..2701
FT /note= "5' end of pZ130 gene"
FT /tag= e
FT /note= "3' end of pZ130 gene"
XX
XX W09640951-A2.
  
```

Alignment Scores:

Pred. No.:	4,21e-06	Length:	3528
Score:	132.00	Matches:	42
Percent Similarity:	33.33%	Conservative:	11
Best Local Similarity:	26.42%	Mismatches:	29
Query Match:	29.66%	Indels:	77
DB:	18	Gaps:	4

US-09-854-562-2 (1-83) x: AAT48816 (1-3528)

```

OY      1 MetAlaArgSerIleTyRheMeAlaPheLeuValIleuA1a---ThrLeuPheValA1a 19
DB      2638 ATGGCTGCTTCATTTCTTCATGCGCATTTTGGTCTGGCAATGATGCTCTTGTGTAC 2697
OY      20 TyrGlyValGlnGly-----
DB      2698 TATGCTTGTCTTCATTAATTTATTCCTAAATCATCGCATTAATAAATATGTAACG 2757
OY      25 LysGluIleCysCysLysGluLeuThyLys-ProValLys-----
DB      2758 AAGCAGACATCAGTAACCGTTTAATTAACCCCTAAATAATTGGAATGATATTACTT 2817
OY      37 -----
DB      2818 GCTATACGTTTAACAACATATGATAAAAAAACCTAAATAATATTCATTTGCTCT 2877
OY      37 -----
DB      2878 CTCATCATGTTATCTAATCTATTTTGTGTGATGATGTAAGAGTGAAGCTCAGCA 2937
OY      38 -----
DB      2938 AATTGCAAGACCAACCAAACTTCCAGATTATGTTTATGACATCATCATGTAG 2997
OY      45 nLysLeuCyMeGluLysGluLeuThyGluAspGlyHisCysPheThrIleLeuSerLy 65
DB      2998 AAAATATTGTATC---AAAGAGAAATTTACTGCTGAGACATGTGTAGCAAACTCCAAAGCA 3054
OY      65 sCysLeuCyMeGluLysGluLeuThyGluAspGlyHisCysPheThrIleLeuSerLy 83
DB      3055 GTGCTATGCACTTAAGCAGCATGTGTTATTTGACAAATCTCAAGTGAAGTTAAAGCA 3109

RESULT 13
AB221971
ID AB221971 standard; cDNA; 3528 BP.
  
```

XX 19-DEC-1996.
 XX 07-JUN-1996; 96W0-US09911.
 XX 07-JUN-1995; 95US-0487087.
 XX (CALJ) CALGENE INC.
 XX McBride K, 'Stalker DM;
 XX WPI; 1997-052341/05.
 XX DNA construct capable of directing ovary-tissue transcription in
 XX plants - useful for modifying colour phenotype, in e.g. cotton
 XX Example 7, Fig 2; 75pp; English.
 XX Calgene Lambda 140 genomic clone (AAT48816) overlaps with the
 XX tomato ovary-specific pZ130 cDNA clone (see also AAT48813) and
 XX includes regions 5' and 3' to pZ130. It was isolated from a
 XX tomato cv. UC82B genomic library using pZ130 as probe. The
 XX genomic clone can be used to construct pZ130 promoter cassettes
 XX useful for directing ovary tissue transcription in plants, e.g. to
 XX modify colour phenotype in cotton.
 XX Sequence 3528 BP; 1191 A; 529 C; 518 G; 1282 T; 8 other;
 XX SQ

XX	AB221971;
AC	
XX	28-MAR-2003 (first entry)
DT	
XX	
XX	Plasmid pZ130 cDNA sequence calgene lambda 140.
DE	
XX	
XX	Transcriptional factor; ovary tissue; gene; ss.
KW	
OS	Unspecified.
XX	
PN	CN189856-A.
XX	
PD	05-AUG-1998.
XX	
PF	07-JUN-1996; 96CN-0195170.
XX	
PR	07-JUN-1995; 95US-0480087.
XX	
PA	(CALJ) CALGENE INC.
XX	
DR	WPI; 2002-733392/80.
XX	
PT	Use of transcriptional factors of ovary tissue -
XX	
XX	Example 5; Fig 2A-C; 56pp; Chinese.
BS	
XX	
CC	The present invention describes the use of transcriptional factors of
XX	ovary tissue. The present sequence represents a nucleotide sequence
CC	which is used in an example from the present invention.
XX	
XX	
SO	Sequence 3528 BP; 1191 A; 529 C; 518 G; 1282 T; 8 other;

Alignment Scores:	
Pred. No.:	4,21e-06
Score:	132.00
Percent Similarity:	33.33%
Best Local Similarity:	26.42%
Query Match:	29.66%
DB:	24
Length:	3528
Matches:	42
Conservative:	11
Mismatches:	29
Indels:	77
Gaps:	4

US-09-854-562-2 (1-83) X ABZ21971 (1-3528)

QY	1	MetAlaAsGSeRlIeTyPheMetAlaPheLeuValIleuAla----	ThrieuPheValIa	19
Db	2638	ATGCGTCGTTCCATTCTTCATGGCATTTTGGCTTGGCAATAGTGCCTTTGTGTACC		2699
QY	20	TyrgIyValGIngly-----		24
Db	2698	TATGCTTTGTCTTCATTAATTATTCCTCTAAATCATCGCATATAAAAAAATGTAAAG		2755
QY	25	LySGluIleCysCysAlaSGIleuThryIys-ProValIys-----		37
Db	2758	AAGCAGACATCAGTAACCGTTTAAATAAACCTTAAAAAATGTGAAATTGATATTACTT		2811
QY	37	-----		37
Db	2818	GCTATACGTTTAAACAATAATGATATAAAAAACCTTAAATAATCTATTTCGATTTGCTCT		2877
QY	37	-----		37
Db	2878	CTCTCATGTTATTCTTAACCTATTTTTGTGTGTGCAATGATTGTAGAGGTAGAAAGCTCAGCA		2933
QY	38	-----		45
		-----CysSerSerAspProLeuCySG1		
Db	2938	AATTGCAAGAAGCAAGCAAGCAAACTTTCCAGAGATTATGTTTATAGGACATCATATGAG		2997
QY	45	nLySeuCySMetGluLySGIleuTyrgIuAspGlyIhIysCysPheThryIleLeuSerIy		65
Db	2998	AAAAATTATTTATC-----AAAGAGAAATTTTACTGCTGGACATTGTACCAAACTCCAAAGAA		3055
QY	65	sCySeuCySMetIySArgCyAsnAlaIySthryIleuAlaThryGluLeuAla		83

DB	3055	GTGCTCATGACCTAAGCAGTGTATTGTAACAAAATCTCAAGTGAAGTTAAAGCA	3109
RESULT 14			
ID	AAQ10263		
AC	AAQ10263 standard; DNA; 4383 BP.		
XX			
XX	AAQ10263:		
XX			
DT	25-MAR-2003 (updated)		
DT	04-APR-1991 (first entry)		
XX			
DE	p2130 contig. Calgene lambda 140 genomic clone.		
XX			
KM	Ovary tissue transcriptional factor; DNA construct; probe; clone p2130; ss.		
XX			
OS	Lycopersicon esculentum UC82B.		
XX			
FH	Key	Location/Qualifiers	
FT	intron	2702..2921	
FT		/*tag= a	
FT	misc_RNA	2599..3382	
FT		/*tag= b	
FT		/label= p2130	
FT		/note= "overlap"	
FT	misc_feature	2567..2567	
FT		/*tag= c	
FT		/label= transcription_start	
XX			
PN	EP409629-A.		
PD	23-JAN-1991.		
XX			
PF	19-JUL-1990; 90EP-0307926.		
XX			
PR	19-JUL-1989; 89US-0382518.		
XX			
PA	(CALJ) CALGENE INC.		
XX			
PI	Martineau B, Houck CM;		
XX			
DR	WPI; 1991-024191/04.		
XX			
PT	New ovary tissue transcriptional factors - modify transcription		
PT	in tomato plant ovaries for use as mol. probes		
XX			
PS	Disclosure; Fig 2; 21pp; English.		
XX			
CC	To prepare pCGN2901, Calgene lambda 140 was digested with SalI		
CC	and the resulting fragment which contains the p27-hybridizing		
CC	region was inserted into pCGN2015, at the unique SalI site.		
CC	pcGN2902 contains the other SalI fragment (non-p27-hybridizing)		
CC	of the p2130 genome derived from SalI digestion of		
CC	Calgene lambda 140 also put into a pCGN2015 construct.		
CC	Plasmid DNA isolated from pCGN2901 was used in the construction		
CC	of a p2130 Promoter Cassette. The promoter is ovary-specific		
CC	and wound-inducible in leaf cells.		
CC	See also AAQ10262-64.		
XX	(Updated on 25-MAR-2003 to correct PA field.)		
XX			
SQ	Sequence 4383 BP; 1539 A; 620 C; 610 G; 1606 T; 8 other;		
	Alignment Scores:		
	Pred. No.:	5.59e-06	Length: 4383
	Score:	132.00	Matches: 42
	Percent Similarity:	33.33%	Conservative: 11
	Best Local Similarity:	26.42%	Mismatches: 29
	Query Match:	29.66%	Indels: 77
	DB:	12	Gaps: 4
	US-09-854-562-2 (1-83) x AAQ10263 (1-4383)		

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Db      2638 ATGGCTCGTTCATTTCTTCATGGCATTGTTGGTGGCAATGATGCTCTTGTACC 2697
Qy      20 TyrGlyValGlnGly----- 24
Db      2698 TATGCTTTGCTCTTCATTAATTTCTCCTAAATCATGCGCATATAAAAAATGTACG 2757
Qy      25 LysGluIleCysCysLeuGluLeuThrLys-ProValLys----- 37
Db      2758 AAGCAGACATCAGTAACCGTTTAATTAACCCCTAATAAATTGGAATTGATATTACTT 2817
Qy      37 ----- 37
Db      2818 GCTATACGTTTAACAATAATGATAAAAAACCTAATAATATTGATTTCGTTCT 2877
Qy      37 ----- 37
Db      2878 CTCATGATTAATCTAATTTTGTGTGTAATGATGTAAGAGTAAGACTACGA 2937
Qy      38 -----CysSerSerAppProLeuCysG1 45
Db      2938 AATTGCAAGACCAAGCAAACTTCCAGATTATGTTTATGACATCATCTAG 2997
Qy      45 nLysLeuCysMetGluLysGluLysTyrGluAspGlyHisCysPheThrIleLeuSerLys 65
Db      2998 AAAATATTGTATC---AAAGAGAAATTTACTGTGTGACATTTGTACCAAACTCCAAAGGA 3054
Qy      65 sCysLeuCysMetLysArgCysAsnAlaLysThrLeuAlaThrGluLeuLeuAla 83
Db      3055 GTGCTATAGCACTAAGCCATGTGTATTGACAAAATCTCAAGTGAAGTAAGA 3109

RESULT 15
AAQ10319
ID      AAQ10319 standard; cDNA; 4383 BP.
AC      AAQ10319;
XX      25-MAR-2003 (updated)
DT      04-APR-1991 (first entry)
XX      Calgene lambda 140 genomic clone.
XX      pZ130; cytokinin; ds.
XX      Synthetic.
OS      9
XX      Key Location/Qualifiers
XX      FH misc_RNA 2567..3382
XX      FT /tag= a
XX      FT /note= "Sequence homologous to pZ130 transcript"
XX      FT misc_RNA 2599..3382
XX      FT /tag= b
XX      FT /note= "Sequence homologous to pZ130 CDS"
XX      FT 2702..2921
XX      FT /tag= c
XX      FT /note= "Sequence homologous to pZ130 intron"

EP409628-A.
XX      23-JAN-1991.
XX      19-JUL-1990; 90EP-0307925.
XX      19-JUL-1989; 89US-0382802.
XX      (CALJ ) CALGENE INC.
XX      Houck CM, Pear JR, Martineau B, Hiatt W;
XX      WPI; 1991-024190/04.
XX      Modulating endogenous cytokinin levels - regulatory regions are
XX      PT transformed into plant cells e.g. fruit to modify pheno-type

```

```

XX      XX
PS      Disclosure; Fig 3; 39pp; English.
XX      CC The sequence encodes an enzyme in the cytokinin biosynthetic pathway,
XX      CC derived from Z130, and useful in modulating a transformed plant's
XX      CC phenotype eg fruit maturation, ripening etc.
XX      CC (Updated on 25-MAR-2003 to correct PA field.)
SQ      Sequence 4383 BP; 1539 A; 620 C; 610 G; 1606 T; 8 other;

Alignment Scores:
Pred. No.: 5.59e-06 Length: 4383
Score: 132.00 Matches: 42
Percent Similarity: 33.33% Conservative: 11
Best Local Similarity: 26.42% Mismatches: 29
Query Match: 29.66% Indels: 77
DB: 12 Gaps: 4

US-09-854-562-2 (1-83) x AAQ10319 (1-4383)
Qy      1 MetAlaArgSerIleTyrPheMetAlaPheLeuValLeuAla---ThrLeuPheValAla 19
Db      2638 ATGGCTCGTTCATTTCTTCATGGCATTGTTGGTGGCAATGATGCTCTTGTACC 2697
Qy      20 TyrGlyValGlnGly----- 24
Db      2698 TATGCTTTGCTCTTCATTAATTTCTCCTAAATCATGCGCATATAAAAAATGTACG 2757
Qy      25 LysGluIleCysCysLeuGluLeuThrLys-ProValLys----- 37
Db      2758 AAGCAGACATCAGTAACCGTTTAATTAACCCCTAATAAATTGGAATTGATATTACTT 2817
Qy      37 ----- 37
Db      2818 GCTATACGTTTAACAATAATGATAAAAAACCTAATAATATTGATTTCGTTCT 2877
Qy      37 ----- 37
Db      2878 CTCATGATTAATCTAATTTTGTGTGTAATGATGTAAGAGTAAGACTACGA 2937
Qy      38 -----CysSerSerAppProLeuCysG1 45
Db      2938 AATTGCAAGACCAAGCAAACTTCCAGATTATGTTTATGACATCATCTAG 2997
Qy      45 nLysLeuCysMetGluLysGluLysTyrGluAspGlyHisCysPheThrIleLeuSerLys 65
Db      2998 AAAATATTGTATC---AAAGAGAAATTTACTGTGTGACATTTGTACCAAACTCCAAAGGA 3054
Qy      65 sCysLeuCysMetLysArgCysAsnAlaLysThrLeuAlaThrGluLeuLeuAla 83
Db      3055 GTGCTATAGCACTAAGCCATGTGTATTGACAAAATCTCAAGTGAAGTAAGA 3109

Search completed; August 23, 2003, 07:11:42
Job time : 218 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: August 23, 2003, 07:04:48 ; Search time 55 Seconds

(without alignments)
666.087 Million cell updates/sec

Title: US-09-854-562-2

Perfect score: 445
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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	438.5	97.6	506	4	US-09-442-631-1 Sequence 1, Appli
2	182.5	41.0	564	3	US-08-984-320-1 Sequence 1, Appli
3	182.5	41.0	564	3	US-08-487-087A-1 Sequence 1, Appli
4	182.5	41.0	564	4	US-08-397-653B-1 Sequence 1, Appli
5	182.5	41.0	564	6	5175095-1 Patent No.5175095
6	132	29.7	3528	3	US-08-984-320-2 Sequence 2, Appli
7	132	29.7	3528	3	US-08-487-087A-2 Sequence 2, Appli
8	132	29.7	4383	4	US-08-397-653B-2 Sequence 2, Appli
9	132	29.7	4383	6	5175095-4 Patent No.5175095
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17	70	15.7	349	1	US-08-543-238-3 Sequence 3, Appli
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ALIGNMENTS

RESULT 1
US-09-442-631-1
; Sequence 1, Application US/09442631
; Patent No. 6300489
; GENERAL INFORMATION:
; APPLICANT: OH, BOUNG-JUN
; APPLICANT: KO, MOON KYUNG
; APPLICANT: SHIN, BYONGCHUL
; APPLICANT: CHUNG, CHANG HO
; TITLE OF INVENTION: SMALL AND CYSTEINE RICH ANTIFUNGAL DEFENSIN AND
; TITLE OF INVENTION: THIONIN-LIKE PROTEIN GENES HIGHLY EXPRESSED IN THE
; FILE REFERENCE: 1942/44
; CURRENT APPLICATION NUMBER: US/09/442,631
; CURRENT FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Capsicum annuum
US-09-442-631-1
Alignment Scores:
Pred. No.: 1.01e-50
Score: 434.50
Percent Similarity: 98.81%
Best Local Similarity: 98.81%
Query Match: 97.64%
DB: 4
Gaps: 1
US-09-854-562-2 (1-83) x US-09-442-631-1 (1-506)
Oy 1 MetAlaArgSerIleTyrPheMetAlaPheValIleAla---ThirPheValAla 19
Db 10 ATGGCTGTTTCATTACTTCTGTTGTTGTCATGCAATGACATGCTTTGTTGCT 69

Qy 20 TyrGlyValGlnGlyLeuGlnLeuCysCysAluLeuThrProValIysCysSer 39
Db 70 TATGGGGTGAAGCAAGCAAAATTTGCTGAAGAGCTCAAAAACCTTTAAATGTTCT 129
Qy 40 SerAppProLeuCysGlnLeuCysMetGlnGlnGlyTyrGlnAlaGlyHisCys 59
Db 130 AGTACCCTCTATGTCAAAACCTCTGATGAGAAAGAAATATGAAGATGCTATTGT 189
Qy 60 PheThrIleuSerLeuCysLeuCysMetIysArgCysAsnAlaIleThrIleuAlaThr 79
Db 190 TTCACAACTCTAAGCAAGTCTTATGATGAGAGATGTAATGCTAAACTCTGGCAACA 249
Qy 80 GlnLeuLeuAla 83
Db 250 GAATGCTTGCT 261

RESULT 2
US-08-984-320-1
Sequence 1, Application US/08984320
Patent No. 6222097
GENERAL INFORMATION:
APPLICANT: McBrider, Kevin E.
APPLICANT: Stalker, David M.
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,320
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/487,087
FILING DATE: 07-JUN-95
APPLICATION NUMBER: USSN 07/998,158
FILING DATE: 29-DEC-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/554,195
FILING DATE: 17-JUL-90
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/382,518
FILING DATE: 19-JUL-89
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 91-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-08-984-320-1

Alignment Scores: 4.04e-16 Length: 564
Pred. No.: 4.04e-16 Length: 564

Score: 182.50 Matches: 41
Percent Similarity: 62.35% Conservative: 12
Best Local Similarity: 48.24% Mismatches: 29
Query Match: 41.01% Indels: 3
DB: 3 Gaps: 3

US-09-854-562-2 (1-83) x US-08-984-320-1 (1-564)

Qy 1 MetAlaArgSerIleTyrPheMetAlaPheLeuValIleuAla---ThrLeuPheValAla 19
Db 40 ATGGCTGTTCCATTTCTTCATGCGATTTTGGTCTTGCAATGATGCTCTTTGTTACC 99
Qy 20 TyrGlyValGlnGlyLeuGlnLeuCys---CysLeuGlnLeuThrIysProValIysCys 38
Db 100 TATAGGTAGAGCTCAGCAAAATTTGCAAGACCAAGCAACCAACTTCCAGCATTTATGT 159
Qy 39 SerSerAppProLeuCysGlnLeuCysMetGlnGlnGlyTyrGlnAlaGlyHis 58
Db 160 TTTATGAGCTCATCATCTAGAAATTTATTTATC---AAAGAAATTTACTGCTGGACAT 216
Qy 59 CysPheThrIleuSerLeuCysLeuCysMetIysArgCysAsnAlaIleThrIleuAla 78
Db 217 TGTAGCAACTCCAAAGCAAGTCTTATGCACTAAGCATGTGATTTGACAAATCTCA 276
Qy 79 ThrGlnLeuLeuAla 83
Db 277 AGTGAAGTTAAAGCA 291

RESULT 3
US-08-487-087A-1
Sequence 1, Application US/08487087A
Patent No. 6268546
GENERAL INFORMATION:
APPLICANT: McBrider, Kevin E.
APPLICANT: Stalker, David M.
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,087A
FILING DATE: 07-JUN-95
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/998,158
FILING DATE: 29-DEC-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/554,195
FILING DATE: 17-JUL-90
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/382,518
FILING DATE: 19-JUL-89
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 91-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 564 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 US-08-487-087A-1

Alignment Scores:

Pred. No.:	4,04e-16	Length:	564
Score:	182.50	Matches:	41
Percent Similarity:	62.35%	Conservative:	12
Best Local Similarity:	48.24%	Mismatches:	29
Query Match:	41.01%	Indels:	3
		Gaps:	3

US-09-854-562-2 (1-83) x US-08-487-087A-1 (1-564)

Qy 1 MetAlaArgSerIleTyRPhMeAlaPheLeuValIleuAla---ThreUpheValAla 19
 |||||
 Db 40 ATGGCTCGTTCATTTCTTCATGCGCATTTTGGCTTGGCAATGATGCTCTTGTATAC 99
 Qy 20 TyRgIValGInGlyLySgIuIleCys--CysLySgIuLeuThrLySProValIyS 38
 |||||
 Db 100 TATGAGGTAGAGGCTCAAGCAAAATTTGCAAGCACCACCAAACTTCCAGGATTATGT 159
 Qy 39 SerSerAProLeuCySgInLySLeuCySMeGluLySgIuLySgIuTyRgIuAspGlyHis 58
 |||||
 Db 160 TTTATGCTCATCATCATGAGAAATATGTATC---AAAGAGAAATTTACTGTGTGACAT 216
 Qy 59 CysPheThrIleLeuSerLySLeuCySMeLySArgCysAsnAlaLySThreAla 78
 |||||
 Db 217 TGTAGCAAACTCCAAAGAAAGTGTATGCACTAAGCATGTGTATTGACAAATCTCA 276
 Qy 79 ThrGluLeuAla 83
 |||||
 Db 277 AGTGAAGTTAAAGCA 291

RESULT 4

US-08-397-653B-1

; Sequence 1, Application US/08397653B

; Patent No. 6329570

; GENERAL INFORMATION:

; APPLICANT: Martineau, Belinda

; TITLE OF INVENTION: COTTON MODIFICATION USING

; TITLE OF INVENTION: OVARY-TISSUE TRANSCRIPTIONAL

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Calgene, Inc.

; STREET: 1920 Fifth Street

; CITY: Davis

; STATE: CA

; COUNTRY: USA

; ZIP: 95616

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB

; OPERATING SYSTEM: Macintosh 7.0

; SOFTWARE: Microsoft Word 5.1a

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/397,653B

; FILING DATE: 28-FEB-1995

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Elizabeth Lassen

; REGISTRATION NUMBER: 31,845

; NAME: Donna E. Scherer

; REGISTRATION NUMBER: 34,719

; NAME: Carl J. Schmedler

; REGISTRATION NUMBER: 36,924

; REFERENCE/DOCKET NUMBER: CGNE 112

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (916) 753-6313

TELEFAX: (916) 753-1510
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 564 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 US-08-397-653B-1

Alignment Scores:

Pred. No.:	4,04e-16	Length:	564
Score:	182.50	Matches:	41
Percent Similarity:	62.35%	Conservative:	12
Best Local Similarity:	48.24%	Mismatches:	29
Query Match:	41.01%	Indels:	3
		Gaps:	3

US-09-854-562-2 (1-83) x US-08-397-653B-1 (1-564)

Qy 1 MetAlaArgSerIleTyRPhMeAlaPheLeuValIleuAla---ThreUpheValAla 19
 |||||
 Db 40 ATGGCTCGTTCATTTCTTCATGCGCATTTTGGCTTGGCAATGATGCTCTTGTATAC 99
 Qy 20 TyRgIValGInGlyLySgIuIleCys--CysLySgIuLeuThrLySProValIyS 38
 |||||
 Db 100 TATGAGGTAGAGGCTCAAGCAAAATTTGCAAGCACCACCAAACTTCCAGGATTATGT 159
 Qy 39 SerSerAProLeuCySgInLySLeuCySMeGluLySgIuLySgIuTyRgIuAspGlyHis 58
 |||||
 Db 160 TTTATGCTCATCATCATGAGAAATATGTATC---AAAGAGAAATTTACTGTGTGACAT 216
 Qy 59 CysPheThrIleLeuSerLySLeuCySMeLySArgCysAsnAlaLySThreAla 78
 |||||
 Db 217 TGTAGCAAACTCCAAAGAAAGTGTATGCACTAAGCATGTGTATTGACAAATCTCA 276
 Qy 79 ThrGluLeuAla 83
 |||||
 Db 277 AGTGAAGTTAAAGCA 291

RESULT 5

5175095-1

; Patent No. 5175095

; APPLICANT: Martineau, Belinda M.; Houck, Catherine M.

; TITLE OF INVENTION: OVARY TISSUE TRANSCRIPTIONAL FACTORS

; NUMBER OF SEQUENCES: 9

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/554,195

; FILING DATE: 17-JUL-1990

; SEQ ID NO:1:

; LENGTH: 564

5175095-1

Alignment Scores:

Pred. No.:	4,04e-16	Length:	564
Score:	182.50	Matches:	41
Percent Similarity:	62.35%	Conservative:	12
Best Local Similarity:	48.24%	Mismatches:	29
Query Match:	41.01%	Indels:	3
		Gaps:	3

US-09-854-562-2 (1-83) x 5175095-1 (1-564)

Qy 1 MetAlaArgSerIleTyRPhMeAlaPheLeuValIleuAla---ThreUpheValAla 19
 |||||
 Db 40 ATGGCTCGTTCATTTCTTCATGCGCATTTTGGCTTGGCAATGATGCTCTTGTATAC 99
 Qy 20 TyRgIValGInGlyLySgIuIleCys--CysLySgIuLeuThrLySProValIyS 38
 |||||
 Db 100 TATGAGGTAGAGGCTCAAGCAAAATTTGCAAGCACCACCAAACTTCCAGGATTATGT 159
 Qy 39 SerSerAProLeuCySgInLySLeuCySMeGluLySgIuLySgIuTyRgIuAspGlyHis 58
 |||||

Db 160 TTATGACTCATCTAGTACAAAATATGTATC---AAAGAGAAATTTACTGTGTGACAT 216
Qy 59 CyspethrilleLeuserlyeCysleucCysmethylsArgCysAsnAlaLeuThreVala 78
Db 217 TGTACCAACTCCAGAGAGAGTGTATGCTACCTAAGCCATGTGTATTGACAAATCTCA 276
Qy 79 ThrGluLeuVala 83
Db 277 AGTGAAGTTAAAGCA 291

RESULT 6
US-08-984-320-2
Sequence 2, Application US/08984320
Patent No. 6222097
GENERAL INFORMATION:
APPLICANT: McBride, Kevin E.
APPLICANT: Stalker, David M.
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,320
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/487,087
FILING DATE: 07-JUN-95
APPLICATION NUMBER: USSN 07/998,158
FILING DATE: 29-DEC-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/554,195
FILING DATE: 17-JUL-90
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/382,518
FILING DATE: 19-JUL-89
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 91-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 basepairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-984-320-2

Alignment Scores:
Pred. No.: 4,228-08 Length: 3528
Score: 132.00 Matches: 42
Percent Similarity: 33.33% Conservative: 11
Best Local Similarity: 26.42% Mismatches: 29
Query Match: 29.66% Indels: 77
DB: 3 Gaps: 4
US-09-854-562-2 (1-83) x US-08-984-320-2 (1-3528)

Qy 1 MetAlaArgSerIleTyrrhemeAlaPheLeuValaLeu---ThrLeuPheVala 19
Db 2638 ATGGCTGCTTCATTTCTTCATGCAATTTTGGTCTTGCAAGATGATGCTTTGTTACC 2697
Qy 20 TyrrGlyValGingly----- 24
Db 2698 TATGTTGCTTCATTAATTTATTCCTTAATATCGCAATAAAAAATGTAACG 2757
Qy 25 LysGluIleCysCysLysGluLeuThryls-ProVallys----- 37
Db 2758 AAGCAGACATCAGTAACCGTTTAATTAACCTTAATAAATTTGTAATTGATATTACTT 2817
Qy 37 ----- 37
Db 2818 GCTATACGTTTAACTAGATGATAAAAAAACCCTAATAATATTACTTATTCGATTTCGTC 2877
Qy 37 ----- 37
Db 2878 CTCTCATGTTATTTCTAATACTATTTTGTGTGTAATGATGTAGAGGTAGAGCTCAGCA 2937
Qy 38 -----CysSerSerAapProLeuCyb1 45
Db 2938 AATTGCAAGACCAAGCCAACTTCCAGATTTATGTTTATGACATCATCATGTAG 2997
Qy 45 nLysLeuCysMetGluLysGluTyrrGluAspGlyHisCysPheThrIleLeuSerLy 65
Db 2998 AAAATATTGTATC---AAAGAGAAATTTACTGTGACATTTGTAGCAAACTCCAAAGAA 3054
Qy 65 bCysLeuCysMetLysArgCysAsnAlaLysThreValaThrGluLeuVala 83
Db 3055 GTGTCTATGCACTAAGCAGATGTATTGACAAATATCTCAAGTAAAGCA 3109

RESULT 7
US-08-487-087A-2
Sequence 2, Application US/08487087A
Patent No. 6268546
GENERAL INFORMATION:
APPLICANT: McBride, Kevin E.
APPLICANT: Stalker, David M.
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,087A
FILING DATE: 07-JUN-95
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/998,158
FILING DATE: 29-DEC-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/554,195
FILING DATE: 17-JUL-90
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/382,518
FILING DATE: 19-JUL-89
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 91-1

TITLE OF INVENTION: OVARY TISSUE TRANSCRIPTIONAL FACTORS

NUMBER OF SEQUENCES: 9

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/554,195

FILING DATE: 17-JUL-1990

SEQ ID NO:4

LENGTH: 4383

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
5,7e-08	132.00	33.33%	26.42%	29.66%	4383	42	11	29	77	4

US-09-854-562-2 (1-83) x 5175095-4 (1-4383)

QY 1 Metalaatgserlletyrphenecalaphleuvalleuala---Thrlauphevala 19
 DB 2638 ATGGCTCGTTCATTTCTTCATGCGCATTTTGGCTTGGCAATGATGCTCTTTGTACC 2697
 QY 20 TyrGlValGlnGly----- 24
 DB 2698 TATGGTTTGTCTTCAATTAATTTATTCCTTAATATCATGCAATATAAAAAAATGTAACG 2757
 QY 25 LysGluileCysCysLysGluLeuThrllys-ProVallys----- 37
 DB 2758 AAGCAGACATCAGTAACCGTTTAAATTAACCTTAATAAATTGGAATGATATTACTT 2817
 QY 37 ----- 37
 DB 2818 GCTATACGTTTAACAACATGATGATAAAAAACCTTAATAATATTGATTTGCTCT 2877
 QY 37 ----- 37
 DB 2878 CTCATCATGTTAATCTAATATTATTTTGTGTGAATGATTGAGTAGAAGCTCAGCA 2937
 QY 38 -----CysSerSerAppProLeuCysegl 45
 DB 2998 AATTGCAAGACCAAGCAAACTTCCAGAGATTATGTTATGACTCATCATGAG 2997
 QY 45 nlyleuCyseMetGluLysGluLysGluAspGlyHisCysPheThrIleLeuSerly 65
 DB 2998 AAAATATTGTATC---AAAGAGAAATTTACTGTGAGCATGTGACAAATCTCAAGGAA 3054
 QY 65 sCyseuCyseMetLysArgCysAsnAlaLysThrlleuAlarhGluLeuAla 83
 DB 3055 GTGCTATGCACTAAGCCATGTGATTGACAAATCTCAAGTGAAGTTAAAGCA 3109

RESULT 10

5177307-1

PATENT NO. 5177307

APPLICANT: HOUCK, CATHERINE M.; PEAR, JULIE R.; MARTINEAU,

BELINDA M.; HIATT, WILLIAM

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

MODULATIONS OF ENDOGENOUS CYTOKININ LEVELS

NUMBER OF SEQUENCES: 6

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/554,196

FILING DATE: 17-JUL-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 382,802

FILING DATE: 19-JUL-1989

APPLICATION NUMBER: 188,361

FILING DATE: 29-APR-1988

APPLICATION NUMBER: 168,190

FILING DATE: 15-MAR-1988

APPLICATION NUMBER: 54,369

FILING DATE: 26-MAY-1987

SEQ ID NO:1

LENGTH: 4383

5177307-1

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
5,7e-08	132.00	33.33%	26.42%	29.66%	4383	42	11	29	77	4

US-09-854-562-2 (1-83) x 5177307-1 (1-4383)

QY 1 Metalaatgserlletyrphenecalaphleuvalleuala---Thrlauphevala 19
 DB 2638 ATGGCTCGTTCATTTCTTCATGCGCATTTTGGCTTGGCAATGATGCTCTTTGTACC 2697
 QY 20 TyrGlValGlnGly----- 24
 DB 2698 TATGGTTTGTCTTCAATTAATTTATTCCTTAATATCATGCAATATAAAAAAATGTAACG 2757
 QY 25 LysGluileCysCysLysGluLeuThrllys-ProVallys----- 37
 DB 2758 AAGCAGACATCAGTAACCGTTTAAATTAACCTTAATAAATTGGAATGATATTACTT 2817
 QY 37 ----- 37
 DB 2818 GCTATACGTTTAACAACATGATGATAAAAAACCTTAATAATATTGATTTGCTCT 2877
 QY 37 ----- 37
 DB 2878 CTCATCATGTTAATCTAATATTATTTTGTGTGAATGATTGAGTAGAAGCTCAGCA 2937
 QY 38 -----CysSerSerAppProLeuCysegl 45
 DB 2998 AATTGCAAGACCAAGCAAACTTCCAGAGATTATGTTATGACTCATCATGAG 2997
 QY 45 nlyleuCyseMetGluLysGluLysGluAspGlyHisCysPheThrIleLeuSerly 65
 DB 2998 AAAATATTGTATC---AAAGAGAAATTTACTGTGAGCATGTGACAAATCTCAAGGAA 3054
 QY 65 sCyseuCyseMetLysArgCysAsnAlaLysThrlleuAlarhGluLeuAla 83
 DB 3055 GTGCTATGCACTAAGCCATGTGATTGACAAATCTCAAGTGAAGTTAAAGCA 3109

RESULT 11

US-08-289-458-1

Sequence 1, Application US/08289458

Patent No. 5608144

GENERAL INFORMATION:

APPLICANT: BADEN, Catherine S., DUNSMUIR, Pamela,

APPLICANT: LEE, Kathleen Y.

TITLE OF INVENTION: PLANT GP2 PROMOTERS AND USES THEREOF

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESS: Steuart Street Tower, One Market Plaza

CITY: San Francisco

STATE: California

COUNTRY: US

ZIP: 94105-1493

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/289,458

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Dow, Karen B.

REGISTRATION NUMBER: 29,684

REFERENCE/DOCKET NUMBER: 12176-4

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 594 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 46..270
US-08-289-458-1

Alignment Scores:
Pred. No.: 0.0137 Length: 594
Score: 84.00 Matches: 25
Percent Similarity: 44.74% Conservative: 9
Best Local Similarity: 32.89% Mismatches: 34
Query Match: 18.88% Indels: 8
DB: 1 Gaps: 3

US-09-854-562-2 (1-83) x US-08-289-458-1 (1-594)

QY 4 SerIleTyrPheMetAlaPheLeuValLeuAlaThrLeuPheValAlaTyrGlyValGln 23
DB 73 ACTATTTCCTTAATGATGCTGCTGCTTTTGTCTATGATGATGCGC----- 120
QY 24 GlyIysGluLeuCyseCysLysGluLeuThrLysProValLys-----CysSerSerAsp 41
DB 121 ---GAGCGAAGAGTCGTGAGCGCTTGACGGCAACTCAAGGGGTTGTGCTTAGTAGC 177
QY 42 ProLeuCyseGlnLysLeuCyseMetGlnLysGluLysTyrGluAspGlyHisCysePheThr 61
DB 178 CGCGATTGTGTAAATGTTTGC---CGTAGAGAGGATTTACCGATGGCTCTTGCAATTGGA 234
QY 62 IleLeuSerLysCyseLeuCyseMetLysArgCysAsnAlaLysThrLeu 77
DB 235 TTCGCTTCAATGCTTCTGACAGAGCCCTGTGCTTAATTAATCTTT 282

RESULT 12

US-08-761-549-1
Sequence 1, Application US/08761549
Patent No. 5981727
GENERAL INFORMATION:
APPLICANT: BADEN, Catherine S., DUNSMUIR, Pamela,
APPLICANT: LEE, Kathleen Y.
TITLE OF INVENTION: PLANT GP2 PROMOTERS AND USES THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,549
FILING DATE: 06-DEC-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/289,458
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 12176-4

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 594 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 46..270
US-08-761-549-1

Alignment Scores:
Pred. No.: 0.0137 Length: 594
Score: 84.00 Matches: 25
Percent Similarity: 44.74% Conservative: 9
Best Local Similarity: 32.89% Mismatches: 34
Query Match: 18.88% Indels: 8
DB: 2 Gaps: 3

US-09-854-562-2 (1-83) x US-08-761-549-1 (1-594)

QY 4 SerIleTyrPheMetAlaPheLeuValLeuAlaThrLeuPheValAlaTyrGlyValGln 23
DB 73 ACTATTTCCTTAATGATGCTGCTGCTTTTGTCTATGATGATGCGC----- 120
QY 24 GlyIysGluLeuCyseCysLysGluLeuThrLysProValLys-----CysSerSerAsp 41
DB 121 ---GAGCGAAGAGTCGTGAGCGCTTGACGGCAACTCAAGGGGTTGTGCTTAGTAGC 177
QY 42 ProLeuCyseGlnLysLeuCyseMetGlnLysGluLysTyrGluAspGlyHisCysePheThr 61
DB 178 CGCGATTGTGTAAATGTTTGC---CGTAGAGAGGATTTACCGATGGCTCTTGCAATTGGA 234
QY 62 IleLeuSerLysCyseLeuCyseMetLysArgCysAsnAlaLysThrLeu 77
DB 235 TTCGCTTCAATGCTTCTGACAGAGCCCTGTGCTTAATTAATCTTT 282

RESULT 13

US-09-127-646-1
Sequence 1, Application US/09127646
Patent No. 6291744
GENERAL INFORMATION:
APPLICANT: BADEN, Catherine S.
APPLICANT: DUNSMUIR, Pamela
APPLICANT: LEE, Kathleen Y.
TITLE OF INVENTION: Nucleic Acids Encoding Plant Group 2 Proteins and Uses
TITLE OF INVENTION: thereof
FILE REFERENCE: 012176-004020US
CURRENT APPLICATION NUMBER: US/09/127,646
CURRENT FILING DATE: 1998-07-31
EARLIER APPLICATION NUMBER: US 08/289,458
EARLIER FILING DATE: 1994-08-12
EARLIER APPLICATION NUMBER: US 08/761,549
EARLIER FILING DATE: 1996-12-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 594
TYPE: DNA
ORGANISM: Capsicum annuum
FEATURE:
NAME/KEY: CDS
LOCATION: (46)..(273)
OTHER INFORMATION: pepper plant Group 2 (Gp2) protein cDNA
US-09-127-646-1
Alignment Scores:
Pred. No.: 0.0137 Length: 594

Score: 84.00 Matches: 25
 Percent Similarity: 44.74% Conservative: 9
 Best Local Similarity: 32.89% Mismatches: 34
 Query Match: 18.88% Indels: 8
 DB: 3 Gaps: 3

US-09-854-562-2 (1-83) x US-09-127-646-1 (1-594)

QY 4 SerileTyPheMetAlaPheLeuValLeuAlaThrLeuPheValAlaTyrglyValGln 23
 DB 73 ACTATTTCCTATATGATGTTGCTGTTTGTCTACTGATATGATGCGC-----120
 QY 24 GlyIysGluIleCysCysLeuGluLeuThrIysProValIys-----CysSerSerasp 41
 DB 121 ---GAGGCAGAAAGATCTGCGAGCGGCTTGACGGGCACTTCAGGGGTTGCTTGTGAC 177
 QY 42 ProLeuCysGluIleLeuCysMetGluIysGluIysTyrglyAspGlyHisCysPheThr 61
 DB 178 CGCGATTGTGTAAATGTTTGC---CGTAGAGAGGATTTACCGATGCTCTTGCAATTGGA 234
 QY 62 IleLeuSerIysCysLeuCysMetIysArgCysAsnAlaIysThrLeu 77
 DB 235 TTCGGTCTCAATGCTTCTGACAGAGCCCTGTGCTTATTAACTCTT 282

RESULT 14

US-09-442-631-3
 ; Sequence 3, Application: US/09442631
 ; Patent No. 6300489

; GENERAL INFORMATION:
 ; APPLICANT: OH, BOUNG-JUN
 ; APPLICANT: KO, MOON KYUNG
 ; APPLICANT: SHIN, BYONGCHUL
 ; APPLICANT: CHUNG, CHANG HO
 ; TITLE OF INVENTION: SMALL AND CYSTEINE RICH ANTIFUNGAL DEFENSIN AND
 ; TITLE OF INVENTION: THIONIN-LIKE PROTEIN GENES HIGHLY EXPRESSED IN THE
 ; FILE REFERENCE: 1942/44
 ; CURRENT APPLICATION NUMBER: US/09/442, 631
 ; CURRENT FILING DATE: 1999-11-18
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 225
 ; TYPE: DNA
 ; ORGANISM: Capsicum annuum

US-09-442-631-3

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
0.0174	79.00	225	22	10	31	8	3
Percent Similarity:	45.07%						
Best Local Similarity:	30.99%						
Query Match:	17.75%						

US-09-854-562-2 (1-83) x US-09-442-631-3 (1-225)

QY 4 SerileTyPheMetAlaPheLeuValLeuAlaThrLeuPheValAlaTyrglyValGln 23
 DB 28 ACTATTTCCTATATGATGTTGCTGTTTGTCTACTGATATGATGCGC-----75
 QY 24 GlyIysGluIleCysCysLeuGluLeuThrIysProValIys-----CysSerSerasp 41
 DB 76 ---GAGGCAGAAAGATCTGCGAGCGGCTTGACGGGCACTTCAGGGGTTGCTTGTGAC 132
 QY 42 ProLeuCysGluIleLeuCysMetGluIysGluIysTyrglyAspGlyHisCysPheThr 61
 DB 133 CGCGATTGTGTAAATGTTTGC---CGTAGAGAGGATTTACCGATGCTCTTGCAATTGGA 189
 QY 62 IleLeuSerIysCysLeuCysMetIysArgCysAsn 72
 DB 190 TTCGGTCTCAATGCTTCTGACAGAGCCCTGT 222

RESULT 15

US-08-793-273C-3

; Sequence 3, Application US/08793273C

; Patent No. 6482410

; GENERAL INFORMATION:

; APPLICANT: Crossin, Kathryn L.

; APPLICANT: Phillips, Greg

; APPLICANT: Prieto, Anne L.

; TITLE OF INVENTION: CYTOTOXIC DERIVATIVES THAT STIMULATE ATTACHMENT AND

; TITLE OF INVENTION: NEURITE OUTGROWTH, AND METHODS OF MAKING SAME

; FILE REFERENCE: BEC00225

; CURRENT APPLICATION NUMBER: US/08/793, 273C

; PRIOR FILING DATE: 1997-05-22

; PRIOR APPLICATION NUMBER: PCT/US95/11684

; PRIOR FILING DATE: 1995-09-14

; PRIOR APPLICATION NUMBER: 08/308,359

; PRIOR FILING DATE: 1994-09-16

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 6049

; TYPE: DNA

; ORGANISM: Gallus gallus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (309)..(5741)

US-08-793-273C-3

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
23.9	70.50	6049	20	8	25	7	3
Percent Similarity:	46.67%						
Best Local Similarity:	33.33%						
Query Match:	15.84%						

US-09-854-562-2 (1-83) x US-08-793-273C-3 (1-6049)

QY 15 ThrLeuPheValAlaTyrglyValGlnGlyIysGluIleCysCysLeuGluLeuThrIys 34
 DB 1296 ACTGCTTCTGCGAGAGGCTACACTGAGAGAC-----TCCGGCGAGCTGACCTGC 1349
 QY 35 ProValIysCysSerSerAspProLeuCysGlnIys---LeuCysMetGluIysGluIys 53
 DB 1350 CCACACAACTGCAACGGCAACGGCGCTGTGAGAACGGCGCTGTGTGTCATGAGGCG 1409
 QY 54 TyrglyAspGlyHisCysPheThrIleLeuSerIysCysLeuCysMetIysArgCysAsn 73
 DB 1410 TTCGTGGGGGATGACTGC-----AGCCAGAAAGGTGCCCGAAGACGTGCAT 1457

Search completed: August 23, 2003, 08:19:24
 Job time : 60 secs